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(54) Title: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI**Field of the invention**

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

10

Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular
35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of
- SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means
10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713 and 715; from *Candida albicans* are defined in SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

- 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),
- 25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- 30 The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term “selectively hybridising” or “specifically hybridising” means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising

- 10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

- The present invention also advantageously provides nucleic acid molecules of at least
15 approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the
20 invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

- The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the
25 sample.

- According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different
30 probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

- Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50
35 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expresssion in host cells, such as a suitable promotor, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

- 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,

5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 35 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- 15 20 25 30

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or the human or mammal homologues thereof can also be used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

- 10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector
- 15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected
- 20 yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said
- 25 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound .

- Alternative methods for identifying compounds which selectively modulate expression or
- 30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

- Another alternative to the above described method comprises (a) contacting a compound to be
- 35 tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which
5 activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or
10 said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the *GAL4* protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide
20 vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a *GAL4* transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent
30 protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

10 All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays. In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* model systems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., 25 *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention. 30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating 35 diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable pharmaceutically acceptable carrier.

15 The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

20 Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%
30 or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and
e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used
5 *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the
15 proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion
20 partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the
25 invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a
10 pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death
15 comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide
20 encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- 25 b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

YGL080W (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

YGR243W (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

YGR183C (QCR9) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

YBR009C (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

Figure 4 Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.

Figure 6. DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.

10 **Figure 7.** Representation of the expression constructs of the synthetic *CaBAX* gene (A) and the *yEGFP-synth CaBAX* fusion (B).

Figure 8. Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synthCaBAX and pGAL1P:GFP-synthCaBAX were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.

15 **Figure 9.** Growth kinetics of GAL1P:synthCaBAX (A) and GAL1P:GFP-synthCaBAX (B) on galactose containing minimal medium.

Figure 10. Immunoblot analysis of two independent transformants of GAL1P:synthCaBAX after 15 hours Bax induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the Bax protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal Bax antibody could be removed by the treatment with *S. cerevisiae* mannan.

20 **Figure 11.** Immunoblot analysis of the GAL1P:GFP-synthCaBAX strain on galactose containing minimal medium. The band appearing at 45kDa represents the Gfp-Bax fusion protein, while the band at 20kDa represents the Gfp protein alone.

25 **Figure 12.** FACS analysis of two independent GAL1P:GFP-synthCaBAX transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the GFP-fluorescence peak is not shaded.

30 **Figure 13.** Viability test synthCaBAX (A) and GFP-synthCaBAX transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.

35 **Table 1.** Oligonucleotides used for construction of the synthetic *CaBAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.

Tables 2- 6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways™ software (Research Genetics).

Table 7. Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

Table 8. Codon usage for the synthetic *BAX* gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax, after linearisation in the Ty
10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse *bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®, Lo Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI FLP* terminator fragment was inserted into
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned
30 into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon
5 membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

10 Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived
15 from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a
20 colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results**25 Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YIpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promotor are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YIpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-
30 containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNApure™ Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNApure™ Reagent was added together with 1 g of glass pearls. The yeast cells
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA
10 pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α -³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α -³³P
15 dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
1 µl 0,1 M DTT
20 1 µl RNase Block (40 units/µl) (Stratagene)
1,5 µl 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 5.10⁸ cpm/µg for both
30 the INVSc1YlpUTyL and the INVSc1 YlpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³²P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 µl polydA (1 µg/ml) and incubated for 24 hours at 42°C
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 µm using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2. Quantification of Hybridisation Signals

20 Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time
25 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H₂O₂-induced cell death
30***The oxidative H₂O₂-challenge***

A preculture of yeast strain INVSc1 containing YlpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³³P dCTP

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YIpUTyL yeast cells.

The specific activity of all probes was $5 \cdot 10^8$ cpm/ μ g.

10

Quantification of Hybridisation Signals

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics, 15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

- Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and 20 INVSc1 YIpUTyL (C) revealed differentially expressed genes. To determine the –fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

- 25 ***Identification of Bax-specific genes within the Bax-responsive pool***

- Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and INVSc1 YIpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background 30 value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YIpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA). Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.
- This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast stains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YIpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Eco*II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression in Candida cells

Strains

The *Candida albicans* strain CAI4 (*ura3^Δ*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *mcrA* Δ (*mrr-hsdRMS-mcrBC*) Δ 80*lacZ* Δ M15 Δ *lacX74* *deoR* *recA1* *araD139* Δ (*ara-leu*)7697 *galU* *galK* *rpsL* (Str^R) *endA1* *nupG*).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
 - 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
 - 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO
 - 20 vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandidaBAX.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

Construction of synthetic *BAX*- and *GFP*-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Stu* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.
- The yeast enhanced *GFP* gene *yEGFP*; (Cormack *et al.* 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 **Creation of the synthetic *BAX* expression strains**

- Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different
- 15 transformants was prepared using the Nucleon[®] extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTCCAGATG-3' (SEQ ID NO 14). Standard
- 20 PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

Western blot analysis

- For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were
- 30 prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an
- 35 anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD₆₀₀ of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in
5 microtitre plates using the Bioscreen C system (Labsystems).

Viability tests

Cells were pregrown in minimal dextrose medium to an OD₆₀₀ of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the
10 time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose
15 containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida*
20 *albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the
yEGFP to allow screening for transformants with a high yEGFP-synthCaBAX expression level
25 using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:GFP-synthCaBAX were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on
minimal galactose medium (inducing conditions). After two days incubation at 30°C all
30 transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently,
35 cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected
5 molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX
10 expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of
15 colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong
20 enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from
25 proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCAGGAAGATCTTCCAATGGTTCCTGGAACAATGGGTTCTGGTGG TCCAACCTCTTCTGAACAAATCATGAAACCGGTGCTTCTTGTTG (SEQ ID NO 3)
A2	TAGAAGCATCTTGTGGTGGTTCCAAGTCAATCTGGGGTTCCAGGCC ATTCTACCAGCTCTATCTTGGATGAAACCTTGCAACAAGAACACC (SEQ ID NO 4)
A3	GGAATTC TCG ACATCAGCGATCATTCTTTGCAATCCATGTTAGAATCCAATTC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTGGTAGAAGCATCTTGTTG (SEQ ID NO 5)
B1	GGAATTCGCTGATG TCG ATACCGATTCTCCAAGAGAAGTCTTCTTCAGAGTCG CTGCTGATATGTTGCTGATGGTAACCTTCAACTG (SEQ ID NO 6)
B2	AATTCTGGGACTTTGGTACACAAAGCTTTCAGAGACCAATTTAGAAGCGAAGTA GAACAAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7)
B3	CAACCTTGATCTT GGA TCAGACCAACAATCTTCTCAAGAAATCCAAGGTC CAACCCATGATGGTCTGATCAATCTGGGACTTTG (SEQ ID NO 8)
C1	ATTGTTGGTCT GGA TCCAAGATCAAGGTGGTGGGAAGGTTTGTGTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9)
C2	TCC CCCCGGGG ATTAAACCCATTTTTCAGATGGTCAAGAAGCGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTTGGG (SEQ ID NO 10)

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

<i>ORF</i>	<i>Gene</i>	<i>Normalised intensities</i>		<i>Up/down</i>	<i>Qvalue</i>
		<i>L</i>	<i>YLB</i>		
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	18932.54	37877.20	↑	2.00
<i>Cellular role : Polymerase II transcription</i>					
YDR253C	MET32	17661.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	73117.62	↑	1.89
YBR289W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.46
YBR089C-A	NHP6B	22698.63	6297.49	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.82	↑	2.70
YMR273C	ZDS1	14699.61	35508.04	↑	2.42
YPL089C	RLM1	34922.91	67856.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30633.33	5250.70	↓	5.83
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	7693.29	18614.99	↑	2.42
<i>Cellular role : Chromatine structure</i>					
YBR009C	HHF1	16668.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12566.96	↓	3.97
YDR224C	HTB1	67355.40	23156.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
<i>Cellular role: RNA processing</i>					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	6381.36	17892.11	↑	2.80
YNL112W	DBP2	9956.84	28036.48	↑	2.82
<i>Cellular role: Energy generation</i>					
YPL078C	ATP4	26902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.86	↓	19.05
YDR529C	QCR7	35346.95	5394.65	↓	6.55
YGR008C	STF2	13275.51	2276.27	↓	5.83
YEL039C	CYC7	13604.38	2689.66	↓	5.06
YKL150W	MCR1	105337.67	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113.966.77	54.014.65	↓	2.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YHR094C	HXT1	12526.90	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32060.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
<i>Cellular role: Signal transduction</i>					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
<i>Cellular role: Protein synthesis</i>					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
<i>Cellular role: Protein folding</i>					
YLR216C	CPR6	9616.80	31126.02	↑	3.24
<i>Cellular role: Protein modification/degradation</i>					
YFR052W	RPN12	5583.57	14855.67	↑	2.66
YDL147W	RPN5	31932.20	52939.11	↑	1.66
YGR132C	PHB1	15429.56	5591.19	↓	2.76
YGR135W	PRE9	39921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.28
<i>Cellular role: Cell stress</i>					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55986.32	33263.12	↓	1.68
YCL035C	GRX1	70248.30	10969.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR48	16670.70	5022.40	↓	3.32
YMR251W-A	HOR7	26879.95	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL064C	PRX1	21525.00	40969.00	↑	1.90
YOL151W	GRE2	2624.55	24152.03	↑	9.20
<i>Cellular role: Unknown</i>					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	YCP4	6869.06	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL109W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7992.40	24164.87	↑	3.02
YJR115W		64690.69	102066.34	↑	1.58
YJL188C	BUD19	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98911.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.69

YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
<i>Cellular role: Cell wall maintenance</i>					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	5.37
<i>Cellular role : Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role : DNA repair/recombination</i>					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
<i>Cellular role : DNA synthesis</i>					
YEL032W	MCM3	23422.85	44327.48	↑	1.89
<i>Cellular role : Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role : Fatty acid metabolism</i>					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
<i>Cellular role : Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role : Small molecule transport</i>					
YDR276C	SNA1	21148.46	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised Intensities		Up/down	Or value
		L	YLB		
Cellular role : Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	64511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.56
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR372C	NDD1	26412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	BOI1	37895.40	57761.52	↑	1.52
Cellular role : Chromatine structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	28801.54	↑	3.79
YOL126C	MDH2	34144.61	65326.97	↑	1.91
YLR327C		97415.94	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR161C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.56	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR345C	HXT3	76352.52	40296.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	RPN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CRS5	2922.32	23848.60	↑	8.16

YLR109W	AHP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21296.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.96	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR243W		30829.66	59765.39	↑	1.94
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19487.41	35273.39	↑	1.81
YDR133C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.46	66537.91	↑	2.37
YLR311C		7803.52	31160.73	↑	3.99
YMR107W		13453.15	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38338.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58016.58	↑	3.40
YOL106W		19917.67	69853.66	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123.84	96824.51	↑	1.07

Table 4: Overview of the differentially expressed genes after 2h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities		Up/Down	Q1 value
		L	YLB		
Cellular role: Protein modification/degradation					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YDL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
Cellular role : Unknown					
YDR202C	RAV2	7483.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	44083.39	↑	1.29
YGR236C	SPG1	16978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.99	↑	1.53
YHR162W		26610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.59	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR069W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.76	11525.24	↓	1.96
YLR311C		11095.31	24660.47	↑	2.22
YJR115W		74757.79	103422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	COS3	24648.97	34895.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YJL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29661.23	↑	1.53
YKR075C		19104.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role : Unknown					
YOL106W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YML128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.69
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	63536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.67	↑	3.92
YIL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS161	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32461.67	↑	1.29
YBL078C	AUT7	16528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8179.94	↑	1.77
YBR149W	ARA1	30706.41	9637.76	↓	3.19
YDR178W	SDH4	14880.91	6237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YDR345C	HXT3	77025.40	56749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41964.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16556.87	↓	1.50
YJL166W	QCR8	15554.30	24509.26	↑	1.58
YHR001W-A	QCR10	12416.35	23465.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.64	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.29	↓	1.56
YGR197C	SNG1	4766.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YOR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities YL8		Up/down	Q1 value
Cellular role : Cell cycle control					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
Cellular role : Cell polarity					
YBL085W	BOI1	32734.79	23497.41	↓	1.39
Cellular role : Chromatine structure					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
Cellular role: Energy generation					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	6.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
Cellular role: Carbohydrate metabolism					
YBR019C	GAL10	3092.50	15697.54	↑	5.08
YDR345C	HXT3	14086.41	25657.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
Cellular role: Signal transduction					
YDR099W	BMH2	63285.16	56028.91	↓	1.13
Cellular role: Protein synthesis					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
Cellular role: Cell stress					
YFL014W	HSP12	40848.44	69781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR173W	DDR48	75407.16	36354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
Cellular role: Unknown					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YKR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.37	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities YLB		Up/down	Q-value
Cellular role: Cell stress					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	29081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.62	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.84	15289.39	↓	5.33
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
Cellular role: Signal transduction					
YDR099W	BMH2	29412.99	58598.42	↑	1.99
Cellular role: Protein synthesis					
YGL147C	RPL9A	13655.66	1585.97	↓	8.61
YGR085C	RPL11B	27465.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.46
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.65
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YDL075W	RPL31A	11969.47	2611.53	↓	4.58
YBL092W	RPL32	7872.80	857.85	↓	9.18
YDL191W	RPL35A	28582.59	6046.25	↓	4.73
YDL136W	RPL35B	25433.49	5064.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.65	↓	4.93
YKR094C	RPL40B	39900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML063W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.60	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.32
YER102W	RPS8B	16234.83	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YOR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR064W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.60	↓	6.68
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	23725.18	11117.26	↓	2.13
YLR167W	RPS31	38648.54	2611.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
Cellular role: Energy metabolism					
YGR183C	QCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.46	37076.83	↓	1.37

YLR038C	COX12	39506.06	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14654.61	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.39	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17862.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
Cellular role : Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
Cellular role : Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHP1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-3.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NHP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.68
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-6.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.66		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.94	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.66
SEQ ID NO 697	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPI1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.99		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.06
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR179W	OYE2	17.58				
SEQ ID NO 217	YIL057C		-31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	QCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL097W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.39			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP40	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML129C	COX14			1.91		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.86			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 691	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 315	YMR251W		-64.41				
SEQ ID NO 317	YMR251W-A	HOR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNR002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	CDC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.76	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR372C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

C. albicans 522 CDS's						S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number	
Ala	GCU	30.7	8686	x	6	21.1	118595	
	GCC	12.7	3582		4	12.6	70785	
	GCA	15.4	4357		2	16.2	91018	
	GCG	2	578		1	6.1	34546	
Arg	CGU	5.9	1682		1	6.5	36518	
	CGC	0.7	204		1	2.6	14571	
	CGA	3.5	989		3	3	16957	
	CGG	0.8	220		3	1.7	9801	
	AGA	23.6	6673		1	21.3	119672	
	AGG	2.7	769		2	9.3	52057	
Asn	AAU	37.9	10731	x	1	36	202351	
	AAC	18.7	5293		2	24.9	140194	
Asp	GAU	43.6	12323	x	5	37.8	212658	
	GAC	14.7	4152		7	20.4	114451	
Cys	UGU	9.7	2757	x	1	8	44797	
	UGC	1.7	493		1	4.7	26357	
Gln	CAA	35.2	9964	x	1	27.5	154529	
	CAG	6.9	1948		8	12.2	68463	
Glu	GAA	49.5	14001	x	3	45.9	257930	
	GAG	11.5	3252		10	19.1	107568	

TABLE 8 - continued

C. albicans 522 CDS's						S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number	
Gly	GGU	33.5	9492	x	2	23.9	134515	
	GGC	4.5	1281		7	9.7	54629	
	GGA	13.7	3874		2	10.9	61481	
His	GGG	7.7	2182		8	6	33627	
	CAU	14	3964			13.7	77260	
	CAC	5.8	1642			7.8	43878	
Ile	AUU	39.9	11281	x	3	30.2	169795	
	AUC	14.2	4005		7	17.1	96126	
	AUA	12.3	3478			17.8	100027	
Leu	UUA	1	295	x		26.3	148133	
	UUG	36.1	10204			27.1	152590	
	CUU	9.8	2777			12.2	68479	
	CUC	2.5	694			5.4	30218	
	CUA	4	1133			13.4	75414	
Lys	AAA	48.6	13760	x	2	42.1	236746	
	AAG	19.4	5477		6	30.8	173174	
Met	AUG	18.4	5219	x	8	20.9	117410	
Phe	UUU	28.6	8100	x	4	26	146355	
	UUC	15.9	4486		7	18.2	102389	

TABLE 8 - continued

TABLE 6 - continued

C. albicans 522 CDS's						S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number	
Pro	CCU	13.2	3722		1	13.6	76366	
	CCC	3.6	1027		5	6.8	38247	
	CCA	26.6	7531	x		18.2	102277	
	CCG	2.4	686		1	5.3	29758	
Ser	CUG	3.1	875		9	10.4	58583	
	UCU	23.3	6595	x	1	23.6	132608	
	UCC	10.3	2928		4	14.2	79928	
	UCA	24.6	6955			18.8	105570	
	UCG	6.5	1836		1	8.6	48186	
	AGU	23.6	6673			14.2	79649	
	AGC	4.5	1269		5	9.7	54330	
Thr	ACU	30.7	8689		1	20.2	113634	
	ACC	13.9	3928	x	8	12.6	70777	
	ACA	17.4	4928		5	17.7	99759	
	ACG	3.6	1019		1	8	44817	
Trp	UGG	11	3115	x	6	10.3	58092	
Tyr	UAU	24	6782			18.8	105489	
	UAC	11.6	3280	x	2	14.7	82483	
Val	GUU	33.2	9391		1	22	123726	
	GUC	10.3	2927	x	3	11.6	65203	
	GUA	8	2265			11.8	66100	
	GUG	10	2842		7	10.7	60033	

TABLE 9: Regulation of 23 selected "Bax-specific" functions

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	8895.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2166.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.69	8655.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	QCR9	23181.54	81865.40	24053.00	3.53
YJL166W	QCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11	0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
 - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by
10 SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c),
and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,
or a nucleic acid representing the complement of any of said nucleic acids as defined in (a)
15 to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid
20 sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
- a) providing (a) genetically modified yeast or fungi according to claim 11,
 - 5 b) treating said genetically modified yeast or fungi with a mutagen,
 - c) isolating resistant yeast or fungal cells, and,
 - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
 - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
 - 20 c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
- a) providing a genetically modified organism according to claim 10,
 - b) expressing a cDNA library in said genetically modified organism, and,
 - 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
- 30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 15 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.

33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.

34. An antibody according to claim 33 for use as a medicament.

35. A pharmaceutical composition comprising an antibody of claim 33 or 34.

36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

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- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

- 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 5 (e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid molecule as specified in a) to f),
- 35 for the preparation of a medicament for treating diseases associated with yeast or fungi.

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs

5 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,
62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
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15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
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628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,
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710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a
25 functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar o any

of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,
26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,
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30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,
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178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,
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- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

- 5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in
10 a pharmaceutically acceptable carrier.
40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically
15 modified yeast or fungus.
41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
- 20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
25 compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel
- 20 pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

25 43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

(d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,

(e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

(a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,

10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),

(c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,

(d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

20 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in frame with a reporter gene,

(b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,

(c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

(a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,

30 (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide encoded by said cDNA library, and,

(c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating an/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 5 69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient
- 10 therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
- 15 71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
- 25 75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
- 30 78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGTATATTAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAATGGTA
GCACGTCGCGTTTATGGCCCCCAGGTTAATGTGTTCTCTGAAATTCGCATCACTTTGAGA
AATAATGGGAACACCTTACGCGTGAGCTGTGCCCCACCGCTTCGCCTAATAAAGCGGTGTT
CTCAAAATTTCTCCCCGTTTTTCAGGATCACGAGCGCCATCTAGTTCTGGTAAAATCGCGC
TTACAAGAACAAGAAAAGAAACATCGCGTAATGCAACAGTGAGACACTTGCCGTCATAT
ATAAGGTTTTTGGATCAGTAACCGTTATTTGAGCATAACACAGGTTTTTAAATATATTATT
ATATATCATGGTATATGTGTAAAATTTTTTTGCTGACTGGTTTTGTTTATTTATTTAGCT
TTTTTAAAAATTTTACTTTCTTCTTGTAAATTTTTTCTGATTGCTCTATACTCAAACCAAC
AACAACTTACTCTACAAC TAATGTCTCTGCCGCCGAAAAGAAACCAGCTTCCAAAGCTC
CAGCTGAAAAGAAGCCAGCTGCCAAGAAAACATCAACCTCCGTCGATGGTAAGAAGAGAT
CTAAGGTTAGAAAAGGAGACCTATTCCTCTTATATTTACAAAGTTTTGAAGCAAACCTCACC
CAGACACTGGTATTTCCCAGAAGTCTATGTCTATTTTGAACCTCTTTCGTTAACGATATCT
TTGAAAGAATTGCTACTGAAGCTTCTAAATTGGCCGCTTATAACAAGAAATCCACTATTT
CTGCTAGAGAAATCCAAACAGCCGTTAGATTGATCTTACCTGGTGAATTGGCTAAACATG
CCGTCTCCGAAGGTACTAGGGCTGTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPASKAPAEEKPAAKKTSTSVDGKKRSKVRKETYSSYIYKVLKQTHPDTGISQ
KSMSILNSFVNDIFERiateASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAATTATGGGCATATTGACCTTCTCCGGTTTCCCTCCCGC
GCTCTCGTATCCGTCTGCATTTGACCTCGAGCAAGCGCTCCACTATGTCTATATGTTTAC
CAGTAAAACCTTCTTAACGTTTGTGATATTTTGAACCTCAACCACATTCAGTATGCGTG
TGTATATAAAGATATTCCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGGTCA
CCCAGGACGAGCAGCGCGGCTATTTTTCTATCATTCCGTGAATAGCGACCAACGGTCGGC
GGCTATTTTTTTTTTTTGCAATTTTTTCGGGATGGGTTCCCCGGCAAAGCTAGCCCCGGA
GATTTTTTAATTACGTAAAGAAACAAGGGGCCGGATGTTGCTGCTATTGGTATATAAAGAG
AGAAGGAGAGATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTT
AAAGAAGCAGGAAGCAAAGGATGTTTAGTAGAATTTGTAGCGCTCAATTAAAGAGGACGG
CATGGACCTTCCCTAAGCAGGCTCACTTGCAATCACAGACGATTAAAACATTTGCCACAG
CACCTATTCTGTGCAAAACAATTCAAACAAAGTGATCAACCAAGACTAAGAATAAACTCTG
ATGCTCCTAACTTTGATGCTGACACAACGGTTGGTAAAATCAATTTTTACGACTACTTGG
GCGACTCTTGGGGGCTTGTCTTCTACCCAGCAGATTTACCCCTGTCTGCACCACCG
AAGTCAGCGCATTCGCCAAATTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTGATCG
GGCTTTCAGTGGAAGATGTTGAGTCCACGAAAAATGGATTCAAGACATCAAGGAAATAG
CAAAGGTTAAAAATGTTGGTTTCCCAATAATTGGTGACACTTTTAGAAACGTGGCATTCC
TATATGATATGGTAGATGCCGAAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG
TGAGGTCTGTTTTCGTCATCGATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTT
CCACCGTCGGAAGAAACACTTCTGAAGTGTTAAGGGTAATCGACGCCTTGCAATTGACTG
ACAAGGAGGGCGTAGTAACCTCAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTC
CCTCTGTCTCCAATGATGAGGCGAAGGCTAAATTTGGTCAATTAATGAAATTAAACCCT
ATTTAAGATTACCAAGTCGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MFSRICSAQLKRTAWTLPKQAHLSQTIKTFATAPILCKQFKQSDQPRLRINSDAPNFDA
DTTVGKINFYDYLGDWSGVLFSPADFTPVCTTEVSFAFLKPEFDKRNVLKIGLSVEDV
ESHEKWIQDIKEIAKVKNVGFPIIGDTRFNVAFLYDMVDAEGFKNINDGSLKTVRSVFVI
DPKKKIRLIFTYPSTVGRNTSEVLRLIDALQLTDKEGVVTFPINWQPADDVIIPPSVSNDE
AKAKFGQFNEIKPYLRFTKSK

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YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTTTAGGTGGCGCGGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACTGGGAG
TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTTCGCAAAGTAT
GTAAGGCGCTGGGTGAGCCCAGCGGACGAGGATGGGCTTAATAAGAACGTACAGTTTAGC
ACAGCTAGAACAGGATACAGCTAAGGGCAACTCTGCTTTTCGGGAGAAGTTAAAGAGGGG
TAGACAATGATGGTAATCTTATAAACC GGCTACAATGAAGGTTGTAGCAGCAAGGAAGAT
GATATTTTAATACGGTTCAGGTGAAATGAAATAGCCGCCCATACGGCATGCTCAAGTTG
TAAGTCAGGACTCTAGCTTTCTACTGTAGTATCCTCTAAAGGACTGCTGTTCTGTGCACC
CCCTTCCTTTGTTTATCATAGCGCACGACAAGAGTACTAATAATTAAGTTAGAACATTA
ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAGCAACCAAAGGAACCAA
AGAAGAGGACCACCAGGAGAAAGAAGGATCCTAACGCCCTAAGAGGCGGTTGTCAGCTT
ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCCGAGAATCCTGACGTAAGTT
TTGGCCAAGTAGGCAGAATATTGGGTGAGAGGTGGAAGGCCTTAAGTCTGAAGAAAAGC
AACCCTATGAATCTAAGGCTCAAGCAGACAAGAAGAGATACGAATCTGAAAAGGAATTGT
ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKRTRRRKKDPNAPKRRLSAYMFFANENRDIVRSENPDVTFGQVGRI
LGERWKALTAEEKQPYESKAQADKKRYESEKELYNATRA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTTCGAAACATCAACTTCTCCTTAATCGACCAACTGACAATGAACTTCAGGTTCTACGAG
AGATCTGCCAATTTCCAGAAGGAAACAATAGGTGGGTAAAGAATGATGCTACAAGATAAG
GATAACTATATCAAAACACTGATGCAACATTTGAAGAAAAAGAGAGTACAAAGTTGATA
AAAGACAGCAAGAATGGCGCCTCCACCTTAACATCTTAACAATTTTCGTTTACTGAAAATG
CTACTAGTATATAATCATTAAAGTATCTAACTATCACTCAATAAAAAATATTATAGATCGCT
TAAAACTCGTTTATTGCCGATTATAAATCCACCAAAGCCGCTCTACCCTTACCTCCGC
CTGGA AAAATTATAATATATAAAGTGAGCCTCGTAATACAGGGGTAAAAAGGAAAGAGGG
GGATATCAAGCATCTGGACTTATTTGCACATCTCCGCCTTCAATTGATAAAAGCGTCTT
GATTTTAATCAACTGCTATCATGTCTTCTTCAGTAGCCTCAACCGAAAACATAGTCGAAA
ATATGTTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATGGTGTTTCGTATCC
CAGCCTGGGTTTGGGGACAGCAAATCCTCACGAAAAGTTAGCTGAAACAAAACAAGCCG
TAAAAGCTGCAATCAAAGCTGGATACAGGCACATTGATACTGCTTGGGCCTACGAGACAG
AGCCATTCGTAGGTGAAGCCATCAAGGAGTTATTAGAAGATGGATCTATCAAAAGGGAGG
ATCTTTTTCATAACCACAAAAGTGTGGCCGTTTCTATGGGACGAAGTGGACAGATCATTGA
ATGAATCTTTGAAAGCTTTAGGCTTGGGAATACGTCGACTTGCTCTTGCAACATTGGCCGC
TATGTTTGTGAAAAGATTAAGGACCCTAAGGGGATCAGCGGACTGGTGAAGACTCCGTTG
ATGATTCGTGAAAAACAATGTATGCTGCCGACGGTGACTATTTAGAACTTACAAGCAAT
TGGA AAAAATTACCTTGATCCTAACGATCATCGTGTGAGAGCCATTGGTGCTCAAATT
TTTCCATTGAGTATTTGGAACGTCTCATTAAGGAATGCAGAGTTAAGCCAACGGTGAACC
AAGTGGA AACTCACCTCACTTACCACAAATGGA ACTAAGAAAGTTCTGCTTTATGCACG
ACATTCGTGTTAACAGCATACTACCATTAGGTTCCCATGGCGCACCAA ACTTGAAAATCC
CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTCACAGGAAATGACTTGCTAATTTCTT
ACCATATTAGACAAGGCACTATCGTAATTCGAGATCCTTGAATCCAGTTAGGATTTCTT
CGAGTATTGAATTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG
AAAAATACCCAGTGAGATTCATCGATGAGCCATTTGCAGCCATCCTTCCAGAGTTTACTG
GTAACGGACCAA ACTTGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTEIYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA
GYRHIDTAWAYETEPFVGEAIKELLEDSIKREDLFITTKVWPVLWDEVDRSLNESLKA
GLE YVDLLLQHWPLCFEKIKDPKIGSLVKTPVDDSGKTM YAADGDYLETYKQLEKIYLD
PNDHRVRAIGVS NFSIEYLERLIKECRVKPTVNQVETHPHLPQMELRKFCFMHDILLTAY
SPLGSHGAPNLKIPLVKKLAEKYNVTGNDLLISYHIRQGTIVIPRSLNPVRISSSIEFAS
LTKDELQELNDFGEKYPVRFIDEPFAAILPEFTGNPNLDNLKY

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YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAACAATCAAGCGGGCCTTTTACTTCGAAGT
GGAGGCTAAGCACCAATAATTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA
ATCTCTTCCAACCATTTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG
AGGACATGTGGTACGAACGCGGGTCCACAGGTGCTTGAAGGAGGGAGCTGTTGCACCTAA
AAGATACTGGAAAATAAGTTTGTCTTTGTATCAGTGATATAGAATGACAAATACATCTA
TTTTGGTTGGGTTGGTAAGGTTTACAGCCTCTGTTGTTGCCAAGTCCTGTTATCGCCAA
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTCAATTTTTCGTCGCATTTAAAA
GAACTGAAATTTCAAACATAAACACCAAAACAAAGCATCATCAAGGGAACATATAGTAA
AGAACTACACAAAAGCAACAATGAATAATCAGCCGCAGGGTACCAACAGCGTTCCAAATA
GTATTGGAAATATATTTAGCAACATTGGAACCTCATCTTTTAACATGGCGCAAATTCGCG
AACAGCTGTATCAGAGCCTCACACCACAACAATTGCAGATGATTGAGCAACGACACCAAC
AGTTACTGAGGAGTCGTCTACAACAACAACAACAACAACAACAACAACAACAACAACA
CGCAAACGCATCAATCTCCACCCCTCCTCCGCAACAATCTCAACCCATTGCTAATCAAT
CAGCGACTTCTACCCCTCCTCCTCCTCCAGCACCACACAACCTTACATCCCCAAATTGGTC
AAGTGCCCTTAGCTCCAGCGCTATTAATTTGCCTCCACAAATTGCTCAGTTACCTTTGG
CTACACAGCAACAAGTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC
AGGTTGTGAATGCAATTACTGTTGCACAACAACAAGTGCAACGCCAAATTGAGCAGCAAA
AGGGACAGCAACCGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGGTTCAGCAGC
AACAGCAGCAGCAACTTAGAAAACCAATACAGCGACAACAGCAACAACAGTTTAGGCATC
ATGTGCAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC
AACAAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAGCAGCAACAACAAC
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT
CTCAGCAAGTTCTCAAGTTAGATCCATGAGTGGACAACCTCCCACCAATGTTGAGCCCA
CTATTGGCCAACTTCTCAACTTCCAAAATTAACTTACCCAAGTACCAAACTATTCAAT
ACGATCCACCAGAAACCAAGCTACCATATCCAACCTATTGGTCAGACAAAAAGCAGATA
CGGATACTTTGTTGTACGAACAAATTATCCAGCGTGATAAAATTAACAAATATTCGCTAA
TAAGAGAAACCAATGGTTACGATCCGTTTAGCATTTATGGATTTAGTAATAAAGAGTATA
TTAGTAGACTGTGGCATACACTGAAGTATTATCAAGATTTGAAGAACTAGAAATGAAAT
CTATCACAAGCACTTCTCAGAAGATTCTTCGGCAAGTATTTGGGGAAATGGTTACTCAG
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCCACAAGTAGAAGTTGGAA
ATAGGAACATTACCTAGAGGATAAATTAAAGTCTATAAACAGGCCATGAATGAGACAT
CGGAACAGTTAGTTCCCATAGATTGGAGTTGATCAAGATCGTGACAGATTCTTCCTCA
GGGACACTTTGTTATGGAACAAAAATGACAAGCTTATTAAAATTGAAGACTTTGTGGACG
ACATGTTGCGAGATTACCGATTTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT
GTCAATCTATACAAGAGCAGATTTCAGGAGTTTCAAGGAAATCCATATATAGAGTTGAATC
AGGACCGTCTAGGCGGTGATGACTTGAGAATTAGAATCAAGCTGGATATTGTCGTGGGAC
AAAACCAGTTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG
AGTTTGCAGAGTCCATGTGTCAAGAATTAGAACTACCAGGTGAGTTTGTGACTGCCATTG
CTCACTCCATAAGAGAGCAAGTTCATATGTATCATAAATCACTGGCACTGTTAGGTTACA
ATTTTGATGGATCAGCGATAGAAGATGATGACATTAGAAGCAGAATGCTCCCAACGATTA
CTCTTGATGATGTTTATAGGCCTGCAGCGGAAAGCAAAATTTTACTCCAAACCTATTAC
AGATTTGAGCTGCAGAGTTAGAGAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA
AAAGAAGACAAGGTAGATCTAATAGACGTGGTATGCTCGCATTTGCCGGCACATCTGCAA
GTAATACATCTATGAACGGCGTTCACAACACAGTAGCAGCAGGAAATGCTTCATCGTTGC
CACCAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGAACTTTCAGGACTCCAG
TACCTAGCACTTTAATGCCTGGTGGTGTGACGTAGGCCCTTCTGTGGAATCGTACGAAT
TGAGAAACACAACCCTTATAAAAGCAGGCCAGATAGACCTAAGCCAGTTTCACCTCCTT
GTTATATTATTGACCATATTCCGGGTCAATTCGCTACTACTTTCTATTAACTGCCTGGGA
AAGTTAATACAAAAGAAGAGTTCGCAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG
CAATGCTTCCGAGTCCAGAATCGCTGAAAACCTAAGCTGAATAGTAACATTCGCGCTGGTG
TGACGATACCTTCAATCCCAAACCCGATTGCCAATCACACTGTTACTAATTCACCCAATC
CCACACTGCAGCCAGTAATCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC
TTCCTATAGCACCTCCAGTAGCACCACATGATAGCGAAGCGACATTGTTGACTAATAGCA
ATAATGGTAGCAGTAACAATAACACACAGAATACATAG

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YBR289W, 905 aa (SEQ ID NO 64)

MNNQPQGTNSVPNSIGNIFSNIQTSPFNMAQIPQQLYQSLTPQQQLQMIQQRHQQLLSRL
QQQQQQQQQTSPPPQTHQSPPPPPQQSQPIANQSATSTPPPPPPAPHNLHPQIGQVPLAPA
PINLPPQIAQLPLATQQQVLNKLRRQQAIAKNNPQVVNAITVAQQQVQRQIEQQKGQQTAQ
TQLEQQRQLLVQQQQQQQLRNQIQRQQQQQFRHHVQIQQQQQKQQQQQQQHQQQQQQQQQ
QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQIQSQQVPQVRMSGQPPTNVQPTIGQLPQ
LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLLYEQIIQRDKINKYSLIRETNGY
DPFSIYGFNSKEYISRLWHTLKYQDLKNTRMKSITSTSQKIPSASIWNGNGYSGYNGGIT
NTTTRVIPQVEVGNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDITLLWN
KNDKLIKIEDFVDDMLRDYRFEDATREQHIDTICQSIQEIQEFQGNPYIELNQDRLGGD
DLRIRIKLIDIVVGQNQLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ
VHMYHKSALLGYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESKIFTENLLQISAAEL
ERLDKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHNTVAAGNASSLPPEILL
PDIADIPTFRTPVPSTLMPGGVDVGPSVESYELRNNTTYKSRPDRPKVPSPPCYIIDHI
PGHSLLSIKLPKVNTKEEFAAAPNDTSSGTNAMLPSPELTKLNSNIRAGVTIPSIP
NPIANHTVTNSPNPTLQPVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN
NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCCCTCCCTCGTTTTAGTTACATAAAATTTACTAATGG
TTGGAATAATTGCGGAAGCTATCACGCGATAACTAGGTACACACGCATTATTTTTATAATC
CCATTATTAATAAATCCGTTATGACCCCTTTTAGTAATAACTTATTAAGAACCTCCGGGTA
AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCCTTCTTGGAACCTAATATAAATAATA
AATTTGCCTAAGGGCATTAGGCCTTACTGCCTTGGCTAGCGTACTTATTTTCGATTTCATAC
AATTTGCACTATTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTACTTGTTTTA
CGTTCATTTTTATTGAGTTTGTAACTTTATCAGAAAGAAAACAAGAAGAGGAAAAAG
GAAAAGAGGGGTCAGGTTAGTATCAATAAAAAAAGAGAGTAAACAAAACAATACAGAC
TCAATTGAAGCACTATAAGAATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGC
ACATAGAGCTTTTAGCCCAAGCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTG
ATATATACAGGGTCGAGGAACTTTACCTGATGAAGTCCTCACCAAGATGAACGCTCCTC
AGAAACCTGAAGATATTCTGTGTCCTGAGAAAACGTTGCTCGAATATGACGCTTTT
TGTTCTGGTGTTCCTCAACTAGGTTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATA
AAACCGGTGGATTATGGGCCAAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTA
GTACTTCCAGTTACGGAGGTGGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTTAG
CTCATCACGGAATTATCTTTTTTACCCTGGGTATAAGAATTCATTTGCTGAGTTAGCCA
GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACCTGACG
GCTCAAGAACTGCGTCTCCACTTGAATTGAGAATTGCTGAAATTCAAGGTAACATTTCT
ACGAAACCGCCAAAAAACTTTTCCCTGCAAAGAAGCCAAGCCCTCCACTGAAAAGAAGA
CCACTACTTCTGATGCGGCTAAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAA
AGAAGGAGGACAAAGGATTATTATCCTGCTGTACTGTCTATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVAAAGGKADIYRVEETLPDEVLTGMNAPQKPEDIP
VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
GQESTVKACLSYLAHHGIIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGPDGSRTASP
LELRIAEIQKTFYETAKKLFPAKEAKPSTEKTTTTSDAAKRQTKPAAATTAEKKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATGAAGGCACATTGTTAATTGAAGAAGAAGAAGAAGAAGAAACAAAATTAA
AACCGATTGACCAATATATGTCTCTGAATGCCAAGGATGGAAATTATTGCAGAAGATTAG
ACTTTTTTTTGTGCAAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA
AAGAGTACAATAGATGGATAAGAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC
ACGGTTTATTTTGAAAAATAATATCCTTCTCGAAAGCTTTAACGAACGCAGAAATTTTCGAGT
TATTAACTTAAAAATACGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAAACCTG
CATAAAGGCATTAAAAAGAGGAGCGAATTTTTTTTTTAATAAAAAATCTTAATAATCATAAA

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AGATAAATAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAATAAA
CTATTATTTTAGCGTAAAGGATGGGGAAAGAGAAAAGAAAAAATTGATCTATCGATTTT
AATTCAATTCAATTTATTTCTTTTCGGATAAGAAAGCAACACCTGGCAATTCCTTACCTT
CCAATAATTCCAAAGAAGCACCACCACCAGTAGAGACATGGGAGATCTTGTCAGTGACAC
CGTACTTCTTAGCGACAGTGGCAGTGTACCACCACCAATGATGACGGTGTACCAGCAG
CAGAGCTCTTGACAACCTTCGTCTAACAAAGCCTTAGTACCAGCAGCGAACTTTTCGAATT
CGAAAACACCTGGTGGACCGTTCCAGACAATGGTCTTAGCCTTTGCAACAGTAGCAGCAA
ACAACCTTTCTAGATTCTGGACCATTGTCCAACCTTGCCAGCCAGCTGGAATACCTTCCT
TGTCAGTGACAGTCTTGGTGTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTCGA
CTGGCAAGACGACTTCGACACCCTTGGCCTTGGCCTTTTCCATCAACTTTGGAACGATTT
CAGCACCAGCCTTGTCGAAGATGGAGTCACCGATTTTCACTGTTTTTCCAAAACCTTCTTGA
AGGTGAAAGCCATACCACCACCAATGATGATAGAGTCGACCTTGTCACAACAGTTGTCAA
TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQFNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV
AVSPPPMMTVLPAAELLTTSSNKALVPAANFNSKTPGGPFQTMVLAFATVAANNFLDSG
PLSNPCQPAGIPSLSVTVLVLASAEKASAMMKSTGKTTSTPLALAFSINFGTISAPALSK
MESPISVFSKTFCLKVKAIPPPMMIESTLSNKL SIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTCGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTTCCTTC
ATGGAAATAGTTTCCAAAAAGTTCTTAGTAATTACCATATGTTCTTGATGTGGCGCTGC
GAAAGAAAGGTTAGCCGACCGGCATCACCCATAATTGTATAATATAGCAATGAAGCAACT
TGTTGAAGTTTTCTTTAAAGTACTATAGTATTGAATAATATCATGTTCACTTGATAAAAT
TGGGTATTTTATTGACCATTATATCGCGTTGGACACTAATGTCTTTCAAGTTGGTGTAC
GTCACGTGCTTTTCAATGTACTGGGGCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG
GCAGATATGATAGGAAGCAGTAACGGCAAGGAAGGATAAGAACATCATTGAGGGAGTCTG
TGGCAGTTTAGCACATGCTTTGGACCATTAAAGGGTTACGTAGAGGAGAAGAGCATATTT
CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCCAGTTTCGAGCATATCGTATG
ATTCGACTACATACGGCACAGCACCGGGCTTGGATATAAAAGAGTTCCAAATCATCGAAG
ATTGGAATGGAAGACCTGCCAGCGCTTGGTGGTGCAGAGGATTGGGCTTCTACAGTCCA
AGATCGAAAAGGTACACGTACAATATTTACCACAATAATAAATATGGGAAGCACAACTTAT
CTAAAGCTGATACCAGGGCATGCTCTCATTCAGTTTCGCTAATGAAACATTCCGGTATGATG
GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTCACCGCAGTAA
ATAATGGAGAAAACACCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG
TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTAGAATTACTT
TGTCCTCGAGAGGTGAATGTTATAACAGGTGAAAAAAGAGGCTGTAGGCGATGCGTTAA
AGAAGGCGTTATTGAGCTTTGAAAAAATCATACTCGATTATGAGACTAAGATTACAAATA
ATTACTATGTCGATGGCTTGATGGCTCAAAAAAATTAATAATGAAGCTAACACCAATT
ACAACCTATTGTGTCAGCGACTAATAGCAAGCCGACTTTTATCAAATTGGAGGATGCTAAAG
GCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSSISYDSTTYGTAPGLDIKEFQIIEDWNGRPASAWSVQRIQLLSKIERITY
NIYHNNKYGKHNLSKLIPGHALIQFANETFGYDGWRMDVIDVEARECQPF TAVNNGENTN
TSEVKYTVVAEAQVKVTLKDGTNTQCGGLGRITLSSRGECYNRSKKEAVGDALKALLSF
EKIILDYETKITNNYYVDGLYGSKKIKNEANTNYNLLSATNSKPTFIKLEDAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTTACGCAATGGCCTTTTTTTTTTTCTTCACGATCATACTCCTTCGCTT
GTCTTTTGGAAATCTTTTTATTCTTACTTTTGACGTTTGTGTTGACCTGTGAGTCCACGGG
CCTTCAAGGCGGCCTTTAAATTCTTAAGTTGTGAACCGGCCATGTATTTGATCTTCCCTT
TTATTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTGCAACCTTCAGATGCTTCT
CGCTAAATGCTCATCTCTAAATTATCATTATTATTCCTAATAAATCCTAAAATTTTTTAC
TCGTTCTGTACGGCTCATCGCCCCAATATTACCCGCTTGTATGTGATCTTTTTGACTTT

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TCGGTGGCAAAATGCAAAGGGGAATCCAAGGAAAAACCATAACAGGACACTACATCAGAG
ATAATCTTGAATTAAGAGAGTAGAGGAATATACTGCTGGGCTCACTACCATTTTTTGTTC
TAGAGTAAACGTAGAGAAAGATGTCAAGAGATGCACCAATTAAGGCTGACAAGGATTATA
GCCAAATTTTGAAGGAAGAGTTTCCTAAGATCGATTGCTCGCTCAAAATGATTGTAAC
CTGCTTTAGACCAACTGTTAGTGTGGAGAAGAAAACCAGACAAGCTTCAGATCTGGCCT
CCTCGAAAGAAGTTTGGCCAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG
ACCTAAATGAGCAATTGACTCTACTCTCAAAAAAGCATGGTCAGTTGAAATTGTCAATTC
AGTATATGATACAAAAGGTTATGGAATATTTGAAAAGCTCGAAATCTTTGGATTAAACA
CCAGAATTAGTGTCAATTGAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG
TGGAAAGAGCTAGGGTCACCAAAGATTGGTGGAAATTAAGAAAGAAGAGGGTAAGATTG
ATGAAGCTGCAGACATCTTGTGTGAGTTACAGGTTGAGACCTATGGCTCCATGGAAATGT
CTGAGAAAATTCAGTTTATATTAGAGCAAATGGAATTGAGTATATTAAAAGGTGATTATT
CCCAAGCCACGGTGCTTCAAGAAAAATTCTGAAAAAACTTTTAAAAATCCAAATACG
AGTCATTGAAGCTAGAATATTATAATCTTCTGGTAAAAATTAGTTTGCACAAGAGAGAAT
ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAAAACAGACGCCATTAAATCAGATG
AGGCTAAGTGGAAACCTGTTTTATCGCACATTGTATATTTCTTAGTCCTTTACCTTACG
GCAATTTACAAAATGATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG
AAAGCCAAGAATCTTTAGTAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAATTG
TTCAAAAAACCTATGAGCCCGTCTTAAATGAGGATGATTTGGCATTGGTGGAGAAGCTA
ATAAGCATCACTGGGAAGATTACAAAAAAGGGTCATCGAGCACAAATTAAGAGTCATTT
CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA
GCCAGACGGAAACATACATCAGTGATTGGTAAACCAGGGCATCATATACGCTAAAGTTA
ATCGCCCAGCCAAAATCGTGAATTTTGA AAAACCAAAAACTCAAGCCAATTATTGAACG
AATGGTCACATAATGTTGACGAATATTAGAACATATAGAAACAATAGGCCATTTAATTA
CAAAAGAGGAAATCATGCACGGTTTGAAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPIKADKDYSQLKEEFPKIDSLAQNDCNSALDQLLVLEKKTRQASDLASSKEVLA
KIVDLLASRNKWDLLNEQLTLLSKKHGQLKLSIQYMIQKVM EY LKSSKSLDLNTRISVIE
TIRVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELQVETYGSMEMSEKIQFI
LEQMELSILKGDYSQATVLSRKILKTFKNPKYESLKLEYNLLVKISLHKREYLEVAQY
LQEIIYQTD A IKSDEAKWKPVLSHIVYFLVLSPYGNLQNDLIHKIQNDNNLKKLESQESLV
KLFTTNELMRWPIVQKTYEPVLNEDDLAFGGEANKHHWEDLQKRVI EHNLRVI SEYYSRI
TLLRLNELLDLTESQTETYISDLVNQGI IYAKVNRPAKIVNFEKPKNSSQLLNEWSHNVD
ELLEHIETIGHLITKEEIMHGLQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAAATAACGCCAGATGCTTTCTATGCTTCTAATCTTTTACCATTTACCTT
TGTTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCCCGACTGGACTAACA
TGCACGTGACATTTTGTGATGGTTTTTCGTCCCTTACTTAGTACGCTTAGTACGCCACAG
TTTATATTTTCTTGACAATAATAAAGAACCTGATTGTGGGTTAGAACTTGCTATACTTTT
AGTTTAAATAAGCAGGAAATAATCTTGAGTTCTGTATCATTATTATAAATAAACTATA
TTTGTCTCTTTGTGCGCCCTCGGAACCTTTCCTCATTACATTGACGAGGTATATATAGATA
TAGTAGATATACATATCTATCCATGGTATATATGTATGCATCTGGATAATTGAATAGGGT
TTCATGTCATATGCCAAGAATTTGTTAATAATATAGTGGA AAAAAGTCAAGAGGTATTAT
AAATTTCAAAAAAGTACCAAATGGAGGATCAGGATGCTGCATTTATCAAACAGGCTACAG
AAGCAATAGTGGATGTATCATTAAATATAGATAACATAGATCCTATAATAAAAGAGTTAT
TAGAAAGGGTAAGGAATAGGCAAAACAGGTTACAAAATAAAAAACCAGCACTCATACCGG
CAGAAAATGGTGTTGATATAAATAGTCAAGGCGGTAACATAAAGGTTAAAAGGAAAACG
CATTACCAAAACCACCGAAGTCCAGCAAAAGCAAACCCCAAGATCGTAGAAATAGTACTG
GTGAAAAAGATTTAAATGTGCGAAATGTTCTGTTGGAATTTTCAAGATCATCAGATTTGA
GAAGGCACGAAAAGACACACTTCGCCATATTGCCTAACATTTGTCCTCAATGTGGCAAAG
GTTTTGCAAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA
GGACTAAATTACTAACTGCGGGTGGTGAGGGTATCAATGAATTACTGAAAAAGTCAAGC
AATCCAACATCGTTTCATCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

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YDR253c, 191 aa (SEQ ID NO 114)

MEDQDAAFIKQATEAIVDVSLNIDNIDPIIKELLERVRNRQNRLQNKKPALIPAENGVDI
NSQGGNIKVKKENALPKPPKSSSKPQDRRNSTGEKRFKCAKCSLEFSRSSDLRRHEKTH
FAILPNICPQCGKFARKDALKRHYDTLTCRRNRKLLTAGGEGINELLKKVKQSNIVHR
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-668 (SEQ ID NO 117)

ACCTTTAGTTCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT
CTCTTGGTAGTTGAGCACAGCATAACAAGAAGCCGCGCGCAAGCGGTAAATGTCTTTCC
TCCGGCCTTCTAACCACCAAAACCGATCTCGGAACATGGGGGGGGGAAGGTCCTCTGAAT
CGAAAAACCCGAGACAGCGAGAGGGATTTTGCAGAAAATTACAAAGATCACTATTTACTG
CTCCCCCTCACTTCCGCAGTCCCCTAATAGCGGAAGATGCAATGGGTGTGGGCTCTGGGTG
CCCTTTAACCACGCCCTCAAAGGGGGTCTGGTTATTTTGCATGGGCGCCTCTATAAA
TACAAAAGAGGAAGTGAGTGTGTTTTGTTTTGGAAGAGGGAAAGGAAAAAAGAAGAAAT
TTACTATCGGTTGTTGTTTTTCGCCAGTATAATACAATTGATTATACATTTTGAACATAA
CAGCACAGCACAAATACAACAATGGATTCTGCCAAGATCATTAACATTATATTATCCCTTT
TCTTACCACCAGTCGCCGTTTTTCTAGCCCGTGGGTGGGGTACTGACTGTATAGTGGATA
TCATTTTGACCATTTTGGCTTGGTTCCCAGGTATGCTATATGCCTTGACATTGTCTCTAC
AAGATTAA

YDR276C, 55 aa (SEQ ID NO 118)

MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILTILAWFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)

AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAATTCTATCGACCTCTCTAA
TATCAAGCACACCACATGGAAGGATTGGGAAAGAATCAACAAGAAGGAATTGCTTCGGGG
CAAAAAGGAACACAAAACCTCGGTCAAAGTTTTTAACTTTTGAAGAGTTGTGGAACGGTGT
AGAAGGCATATAAAATAGATCGTTAATATATTTCTAACATCTTCTTGTAATGTAAATAT
TTTAAAAGGGTTGATCTTATTACGGAGAGAACCAATCATATCGAAGGATTTCTCAATAGT
AAGTATCCCCGCGCGTGGTCCCTCGGGGAAATAGAACGAGAACTTCAAGTACTTGATAGCA
AAGAAAGTGAAGTGTGTTGAAATTGTTCCAGAACTTTCATTTAAAGTCTTTCGTGAAAGGA
GTGGACGTCAAAAAGAAATAATGATTTTTTAAACGTGCAGTATCTACATTGATTCTCCAA
AAGTTGTGTCTTCCAAGAATATAGGTTCCGCCACCAAATGCCAAGCGCATTGCTAATGTTG
TTCACTTTTATAAGTCTTTGCCTCAAGGACCAGCACCAGCCATCAAGGCTAACACTAGAT
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTTGTGGC
ATTTTGCTCTAGGTATAATTGCCTTTGGCTATTCCATGGAATATTATTTTCATTTGAGAC
ATCATAAAGGTGCGGAAGAGCATTTGA

YDR377W, 101 aa (SEQ ID NO 128)

MIFKRAVSTLIPPKVVSSKNIGSAPNAKRIANVVHFYKSLPQGPAPAIKANTRLARYKAK
YFDGDNASGKPLWHFALGIIAFGYSMEYYFHLRHHKGAEH

YEL039C, 842 bp, CDS: 501-842 (SEQ ID NO 141)

AGTAATTGTCTCCCATTTTTTGGTATACGAGCTAGCAGGACCTTTTGCCCAATGACCATT
CATATTTCATCCCACTCACCACCGTCATCGTTGGTATTATTATTATCATTCCGCTTGAAGA
AAAAGAAACGAAAAAAGAAATGGATCAGCAGCCGGGTATAGCGCCCCTTATTGAATTAT
TTTCCTTCGTGCCTTCTCTGAGAAGGGTCTGCAGTCCCCCGCCGAGGGGTCTTTTCCCAC
CTTCTCAAAGCTAATAGCGATAATAGCGAGGGCATTTATTCAAGTTCCAACACTATAAG
TGGCCGCAAGGGGCAAAGACAAAGGCACACAACATATATATATATATCGTGTGTGAAGCTC
GAGAAGATTAGATCAGAATAGTTCTCTTTTTTGTGAGGTTGAAACAAAATCAAAGACTTA
TACAAGAAGATCACATACAAGCATTTATTACATTACTTTAAGTAACTTCAGTAACTA
CATTACATCATAAACAAAACATGGCTAAAGAAAGTACGGGATTCAAACCAGGCTCTGCAA
AAAAGGGTGCTACATTGTTTAAACGAGGTGTCAGCAGTGTACATAATAGAAGAGGGTG
GTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTTGGTAGACATTTCAGGTCAGGTAA
AGGGTTATTCTTACACAGATGCAAACATCAACAAGAACGTCAAATGGGATGAGGATAGTA

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TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTATATGACAAAGGCTGCCAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD
ANINKNVKWEDESMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCTTTTATTTTAGGCTCTAAAATAACCATGGACA
ACGTGAATTGGGTAGCATCTTTTTTTTAATAGATAGTTTATTATGTATAACAATAATTTA
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTCCTTTACCG
CCAGTTTCTGTACTATGAAAAAGGCAAATTCGCATTGTAGCCGCCACACGCATTTTG
ATCATCAATTACGAAATTTGCCGCACACGTGTCACGTGATAAGCACTCTTACTATCATGT
TTTACGGAGTAGCAATGATGTTCAATTATTGCAGCTTCTTTTCGTGAAATCGTAGTATCA
TAGACCTTCCTAATGATGGAAGCGGTAAAGAAGGAAATCGTAAAAGTAAATTAACGAAGT
AGTATTAGTAAAACAGAGTTGAAAACTGATAAATCTTCAACTCGAACTGAAAAGAAACA
CAATAGAATATTTTTTCTCAATGCTACCTTTTATATCTTTTAAACAAATGCGAAGGGACAAC
AAATGCAAAATAGAATTGAAAAACGGTGAAATTATACAAGGGATATTGACCAACGTAGATA
ACTGGATGAACCTTACTTTTATCTAATGTAACCGAATATAGTGAAGAAAGCGCAATTAATT
CAGAAGACAATGCTGAGAGCAGTAAAGCCGTAAAAATTGAACGAAATTTATATTAGAGGGA
CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTGACAAGGTCAAGCAGCAAAATTA
ACTCCAACAATAACTCTAATAGTAACGGCCCTGGGCATAAAAAGATACTACAACAATAGGG
ATTCAAAACAATAAGAGGTAAC TACAACAGAAGAAATAATAATAACGGCAACAGCAACC
GCCGTCCATACTCTCAAACCGTCAATACAACAACAGCAACAGCAGTAACATTAACAACA
GTATCAACAGTATCAATAGCAACAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLYLLTNAKGQQMQIELKNGEIIQGILTNVDNWMNLTL SNVTEYSEESAINSEDNAES
SKAVKLNEIYIRGTFIKFIKLQDNIIDKVKQQINSNNNSNSNGP GHKRYNNRDSNNNRG
NYNRRNNNNNGNSNRRPYSQNRQYNNNSNSSNINNSINSINSNNQNMNNGLGGSVQHHFNSS
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAAAATTTCAACGGTGGTGTCTTAATGGTTTCCCATGATATCTCTGTTATTGACTCTGT
TTGTAAAGAGATTTGGGTTTCAGAGCAAGGTACTGTCAAGAGGTTTCAAGGTACAATTTA
CGACTATAGAGATTACATCTTGCACTGCTGATGCTGCAGGTGTGGTTAAAAAGCATTG
ATTATTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTAAGTATGCATTC
ATAGCCCCATGATACTTTTTTTTTTGACTACTTGTATTGGAATCTAATTGACCTAACTGG
GCATTCTGGGTCAATTGGTATATGTATCACTTTTTACGTAAAAAAGTAGTGGCTAATATAA
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTTCGAATTTTGCCACTGCAAGTAATTGG
TGCAATTGAAATACGAGATTTTCTTCTAAGAGGATATAAAAATAAGGAAATTAGCCCT
ACCTATCCTTGTGTTAAAATATGAGCGGAGAAACGTTTGAGTTCAATATTAGACATTCTG
GTAAAGTTTACCCAATAACACTTTCCACTGATGCTACTTCAGCAGATTTGAAAAGCAAAG
CAGAGGAATTGACCCAAGTCCCAAGTGCCCGCCAAAAATACATGGTTAAAGGTGGCTTGT
CTGGCGAAGAGTCCATTAAAATATATCCCTTAATCAAGCCAGGATCGACAGTAATGCTAT
TGGGGACTCCAGATGCTAACCTGATTTCTAAACCAGCCAAAAAGAATAATTTTCAATGAAG
ACCTTGCGCCTGAGCAACAAGTCCAACAATTTGCTCAATTGCCTGTTGGTTTCAAGAATA
TGGGCAACACCTGTTATCTGAATGCTACCTACAGGCTTTATACAGAGTGAACGATTTAA
GGGATATGATTCTTAATTATAACCCTTCTCAAGGTGTGTCTAACAGTGGTGCACAAGATG
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTGTTTTGAAAATTTACAGAATA
AAAGTTTCAAGAGTGTTTTGCCAATTGTGTTATTAAACACGCTAAGAAAGTGTTATCCAC
AATTTGCTGAACGTGATTACAAGGTGGGTCTATAAACAGCAAGACGCTGAGGAGTTGT
TTACACAAC TATTCATAGTATGAGTATTGTTTTTGGTGACAAATTTTCCGAAGATTTCA
GGATTCAATTTAAACTACCATCAAAGACACAGCTAATGATAACGATATTACTGTAAAG

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AAAATGAAAGCGATTCTAAATTACAATGTCATATTTCTGGTACTACAAATTTTCATGAGAA
ATGGGCTCCTGGAAGGTTTGAATGAGAAAATTGAAAAAGATCAGACTTGACTGGCGCCA
ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTACCAAAGTTTTTAAGTGTTCAGT
ACGTTAGATTTTTCTGGAAAAGGTCAACCAACAAAAATCTAAAATATTGCGTAAGGTCG
TTTTCCCATTTCAATTAGATGTTGCAGACATGCTTACCCAGAATACGCAGCAGAGAAGG
TAAAAGTTCGTGACGAAGTGAAGAAAAGTGAAGAGGAGAAAAATGAAAAGGAAAGAGAGA
TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAAT
ATGAGACACAAGTGGCTCTTAACGAAAAGTGAAGAAAAGATCAATGGCTCGAAGAGTATAAGA
AACATTTTCTCCAAACTTGGAAGAAAAGTGAAGAACCCATCTTGTGTTTATAACTTGATCG
GTGTCATTACACATCAAGGTGCCAATTCTGAGTCTGGACACTATCAAGCTTTCATAAGGG
ACGAAGTGGACGAAAATAAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTGAAA
AGGAAAAAATTGAATCTTTAGCCGCTGGGGGCGAAAGTGATAGTGCAGTGCATCTTAATGT
ATAAAGGATTTGGTCTGTAA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSKEELTQVPSARQKYMVKGGLSGEESIK
IYPLIKPGSTVMLLGPDPANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNCTYL
NATLQALYRVNDLRDMILNPNPSQGVSNSSGAQDEEIHQIVIEMKRCFENLQNKSFKSVL
PIVLLNLTNRKCYQFAERDSQGGFYKQQDAEELFTQLFHSMSIVFGDKFSEDFRIQFKTT
IKDTANDNDITVKENESDKLQCHISGTTNFMNGLLEGLNEKIEKRSDLTGANSIYSVE
KKISRLPKFLTQYVVRFFWKSTNKKSKILRKVVFPFLQDVADMLTPEYAAEKVKVRDEL
RKVEKEKNEKEREIKRRKFDPSSENVMTPREQYETQVALNESEKDQWLEEYKKHFPNPL
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDELLENKWKFNDDKVSVEKEKIESL
AGGESDSALILMYKGFG

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTAATTCAAGTGATGAGGCGGAAACGTGCAAGATCCTAAATGAAGGAT
AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTAGAAAAACCGAAAAGACAAC
TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC
CTGGAACACGCATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAGTTTCG
ACAATTGCTCGCCTTTATAAGCCATGCTAGTGCCCAATCAAACTTTACTTGCCCTGAA
TTTCCTTTTTTTCTAGCCTGTAACCTTAAATAAGCCATCTAACCTTTTTTTCTAAAAAT
TTTCTTTATTACCCTGTCGGCTTATTTCTATTCTACACATTATTTGCCACCCATTGAAA
TTGTAGCTTGTATTAATAGGGAAAAGCCGGAAGTATAACCGGTGGAAGTACTATTGAAG
TGAGATAAGAAGCCATCGTAATGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG
CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC
TTATCAAGAATAACCTTTTAATACCTGACTTATCCATTCAAAATGACATCTATTTGAATG
ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCATCCAACTTTCA
ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCCTTACTACTTTAGCAACAATC
ATAAATTATCTGAATCTGACAAGAAATCGAAGCTGATAAGTCTGTATTTGTTGAACCTAT
TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACATATCA
AGAACTTGGAAGACGATTCACTTTTGTCTTACCCTATCAAAGTAGACAGATGGCTCATGG
AAGGGTCGTACCAGAAAGCATGGGATCTTCTGCAATCTGGGTGCGAGAATATATCAGAAT
TCGACTCTTTTACCGATATCCTAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG
AGCTATCCTACGACTTTCTCCCTCTCTCAACATAAAGGCTTTGCTCTTTTCAACAACG
AAAAAGAACTGAAAAATTTGCACTAGAGAGAACTGGCCTATTGTCAACTCGAAAGTTT
ACTTCAATAACCAATCAAAGGAGAAAGCTGATTACGAAGATGAAATGATGCATGAAGAAG
ACCAAAGACAAACATTATCGAAAAAGCAATGGATTATGCCATAAGTATTGAAAATATTG
TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MPSLAELTKSLSIAFENGDYAAACEKLLPPIKIELIKNNLLIPDLISQNDIYLNLMITKR
ILEVGALASIQTFFNDSFENYFNQLKPYFYSNNHKLSESDKSKLISLYLLNLLSQNNTT
KFHSELQYLDKHIKNLEDDSLSYPIKLDRLMEGSYQKAWDLLQSGSQNISFDSFTDI
LKSAIRDEIAKNTELSYDFLPLSNIKALLFFNNEKETEFALERNWPIVNSKVYFNNQSK
EKADYEDEMMEEDQKTNIEKAMDYAI SIENIV

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>YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCTGTCTGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT
AATAGGTAATACTTTTGTAACTGTAAAGAATATTAAATCGTTTTTCACGGAATTGGCCTC
TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACCTCAACCTGTGAAAGT
TATGTAATATGCGAATTCTGTTTCTGCTTGATAATCTGAAGAATATAGTCTCGAGCACGC
GATGGAGCAGAAAGGGGAGAAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC
GTTTCTCTTGATTACCTTTTCATCCAACAGTCAATATAAGTACGCCAACTTGCGTTAAAA
CGGCCAATGTGACACCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA
ACGAGAACTCTTCACGACTCATCTACTTGGCATTTCCTGGGTGCAGTTCAACCTCACTCG
CGTGGCGGCGGTGTGAGGTGCATGGGTGCCGGTATTTTCTTTAGTTTCGCTCTGCGCCTTAC
GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC
CCTGTGTACTATTTCTTAGCTCGTTTGGGCAGGCGGTGATCGTTGTACTCTGTGCGGTCC
TGTATTTTCGACTATAGCCGGTCCGGTATTTCTCCACAAATCTTTCTTAGCGTTCTCG
GGCGCCGTGTGCGCTGGGTGGAATAACTGTGGTCATTAAAGCTTGGCAGGTTATCACTC
ACTTTAGTGTTTTCAGTGGCGCTGAACCTTTATATCGGGGGACACCTTGTACTTCCCTCA
CTAGTGTATTGTCTGTTTAG

>YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLCALRDQLREHTILNDYIRYLMTLPCVLFLSSFGQAVIVVLCRVLYFDYSR
FRYFLHKSFLSVLGRRVGLGGITVVIKAWQVITHFSVFSGAELYIGGHPCTSLTSVIVV

>YGL080W, 893 bp, CDS: 501-893 (SEQ ID NO 161)

GAAGAAAAAGAAGAGGGGATGATGAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA
AAAAGAATAAAGGGCAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG
AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTACTACTAATAGTAATCTTGATT
TTTGACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCATATTGTCTGGGTG
GTATTATAGCTTCATGGCTAGTCAAATAAGTGGAGTTTTTTGCTCTGGACGTGGCCTGTA
AAGTTCTCTTTTGCAGCGGCCCGCTTTAACCGAGGCGAAATGACAAGTGCTTTCTGG
CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATTT
AAACTCACTTGCCAATCAGCAAACGTCAATACATCTACATATATACGTATAGATTTTA
TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCAGCACGCTCATTCC
TTCAAAAATACATCAATAAAGAACTTTGAAATATATTTTCACAACACACTTCTGGGGTC
CCGTATCAAATTTCCGGTATCCCAATTGCTGCTATATATGATCTGAAAAAAGACCCTACAC
TAATCTCTGGCCCAATGACTTTTGTCTTAGTTACCTATTCAGGTGTTTTTCATGAAGTATG
CTCTTTTCAGTATCACCCAAAACTACTTACTGTTTGGATGCCACCTTATTAATGAAACTG
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAATACACGTATTTTCACAACAGATGAGGAGA
AGAAAGCTCTAGATAAGGAATGGAAGAGAAAGAAAAAACTGGTAAACAGTAA

>YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAAARSFLQKYINKETLKYIFTTHFWGPVSNFGIPIAAIYDLKKDPTLISGPMT
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQGYRFLKYTYFTTDEEKKALDKE
WKEKEKTGKQ

>YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CGCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAGATAAAAGATAAA
AGATAAAAGACAAAAGAAAATTCATAGCCCATGTTGAAGTATCCCAGCGGGAAATGTTGC
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAATTAAGTGATGCTATCCG
TCCCACAATAATTTTCTCCAGCGGAGGAAATATACGCGGAGGGGGGAGGAAAACCTCT
CAGTAAGCAATGAAGGGATAGATAATGGGGGCGCGCTGCCTAGCTTAGGCTAAGAACT
CCTTCGAAAACAGGGGGCTGCGAGCGCAGAAGCGAACACTTGTCAATTTGTATAAAAGGAC
TATTTATAAGTTTGTCTTTTGTCACTCTCTTGGCCCTAATTACCCATACTATTGTAACAA
TTGTTGTGTAACTCAATTATACAAATAAACGAACAATCAACAGTAACAAACCGCTCAAG
TGTACAACCAATCAGAAAAAATGACGAGAACAAACAAGTGGACCGAACGTGAAGGAAAGG
CTGATCCAAAGTACTTTTCGCACACTGGTAACTACGGTGAATCTCCAAATCACATCAAGA
AGCAAGGTTCCGGCAAGGGTAATTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTG
ATAATGGTGAAATACCCCCAGTGTTCAAGAAAGATAGAAGAGGCTCAAATTTGCAATCGC

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ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

>YGR008C, 84 aa (SEQ ID NO 166)

MTRTNKWTTEREGKADPKYFSHTGNYGESPNHIKKQSGSGKGNWKGPGDEIDDLIDNGEIPP
VFKKDRRGSNLQSQHEQKFENVQKE

>YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGGATCTGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA
ACACCAGGATGAAC TAAGGGCTCATCTCGAAAGTCAAGGTGCCTCATT CAGGTTATTAG
TGGTGCCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTACTTGTTGTTGCATGAGAT
ATCATTTTTTTTTTCCCTCTTTCTTGGGGTCTTGACAGTCATCAAATCGAAGTTT TAG
TTTTTCTTCTTCGGGAAGATCAATTTTAGGTAGAAAAGTGTAGATGAAAAACGAAGGATA
CTGCTATTTACTGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA
TATTCGAGGAGATAATTGGGATATAATCC'TCCATTGCTTCCGAAATTTGTTTAAACACT
TCTAGTTCATTTTCGGGTGGTTCGATCTTCGTTTCCACTTTTAACTTACTCCCAGTTAGT
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT
CAAGCCTATCTATGTGGAGAACGATTCTCATGGCGTTAACAACACTACCGCTAAGTGTTT
TTTCGCAGGAGTTGGTTCAGCTAATAGCACAAACATCGAGCACAGCTCCTTCCATCACTT
CGCTTTCGCGAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAT
CAACGCCGAGTATAGCTTCAGTATCCTTTACTTCCCTTCCACAAAGTTCTTCACTGCTTA
CTCTTTCGTCAACATTATCCTCAGAACTTTCCCTCTTCGTCCATGCAAGTTTCGTGCTCTT
CAACATCGTCGTCTTCTTCGGAGGTTACGTCATCATCGTCATCATCAATATCTCCTT
CCTCTTCATCATCAACAATAATATCATCGTCATCATCACTGCCGACATTCACTGTGGCAT
CAACATCTTCGACAGTTGCCTCCTCCACACTTTCCACTAGCTCATCGTTGGTTATCTCTA
CGTCTTCGTCAACGTTTACGTTTAGTTTCGAAAGTTCAAGCTCTTTGATTTCTCTTCAA
TTTCAACATCCGTTTCGACTTCTTCAGTGACGTTCCCTCCTCTTCAACTTCATCTCCAC
CTTCGTCTCATCCGAATTGACATCATCCTCGTACTCATCATCCTCATCCTCATCCACCC
TCTTTTCTTACTCCTCCTCATTTTCATCATCCTCATCCTCATCCTCATCCTCATCCTCTT
CATCCATATACTCGTCTTCGTATATCCTTCATTTTCATCTTCATCTTCCCTCAAACCCTA
CCTCATCAATCACTTCTACATCCGCTCATCTTCTATTACTCCCGCTTCCGAATATTCCA
ATT TGGCAAAAACCATAACTAGTATAATAGAAGGCCAGACCATCCTCTCTAACTACTATA
CCACAATAACGTATTCACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG
GCTTATCAAAAAGAATCGTAATATTATCATCGGTTGTGTGGTTGGCATAGGTGCCCCCC
TCATCCTAATTCTACTAATATTGATTTACATGTTTTGTGTT CAGCCTAAAAAACGGATT
TCATTGACTCTGACGGTAAAAATTGTCACAGCTTATCGTAGTAACATTTTCACCAAAATAT
GGTATTTCTTGCTGGGTAAAAAATTGGTGAAACAGAAAGATT CAGCTCAGATTTCCCCCA
TCGGCAGCAATAATATT CAGAATTTTGGTGATATCGATCCAGAAGATATACTTAACAATG
ACAACCCCTACACCCCTAAACACACTAATGTTGAAGGCTACGACGACGACGACGACG
ACGCTAATGATGAAAACCTATCATCCAATTCCATAACAGAGGCATAGATGATCAATACT
CACCTACTAAATCTGCATCATATTCAATGTGCAATAGTAATAGTCAAGATTACAACGACG
CAGATGAAGTAATGCACGATGAAAACATTCATCGTGTATGATGACAGCGAAGCTAGCA
TCGACGAGAACTATTACACGAAACCAACAACGGCTTAAATATCACGAAC TATTAA

>YGR023W, 551 aa (SEQ ID NO 168)

MASCNPTRKKSSASSLSMWRTILMALTTPLSVLSQELVPANSTTSSTAPSITSL SAVES
FTSSTDATSSASLSTPSIASVSFTSFPQSSSLTLSSTLSSELSSSSMQVSSSSTSSSSS
EVTSSSSSSSISSSSSTIISSSSLPTFTVASTSSTVASSTLSTSSSLVISTSSSTFT
FSSESSSLISSSISTSVSTSSVVPSSSTSSPPSSSSELTSSSYSSSSSSSTLFSYSSS
FSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSIYSSSYPSFSSSSSNPTSSITST
SASSSITPASEYSNLAKTITSIIEGQTILSNYYTTITYSPTASASSGKNSHHSGLSKKNR
NIIIGCVVGIGAPLILILILLIYMFCVQPKKTD FIDSDGKIVTAYRSNIFTKIWYFLLGK
KIGETERFSSDSPIGSNNIQNF GDIDPEDILNNDNPYTPKHTNVEGYDDDDDDANDENL
SSNFHNRGIDDQYSPTKSASYSMSNSNSQDYNDADDEVMDENIHRVYDDSEASIDENYYT
KPNNGLNITNY

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>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2: 880-1244 (SEQ ID NO 169)

TATAAAAAAAAAATCTTGTAGACAATAAAATAAGAAATGCCCATTTTGTAACTTAGCGAAA
GATGCCCAGTACATCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTTAATAGGAGCT
TTATCATATCTCTTGTATTTTTTTCTGCTGTCTCGGCTTGAGGGACTCACAGAGATCT
GGAAATTTTCAGATTGTCAGTGCCTTAGGATGGGTTGTCAGTAGACGGTGGCCGCCGTGGA
TGGGAAATCTCATACGTTTACACACATAGTGTTTGGAAATTAATAGTAGCAATAGCTATC
TGGCTACTGTTTTAAAGTATTAGCCCGTTCTCAGTGCCTCTTTTTTAAGGAATAACAACG
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG
AATAACGATAGAAAACATGAGTGAATTTCCGTCCACGAAAAAATGTTAACATAAAATGCA
AGAGAACAATTAATCGAATAATGTTAAATTATTGTAAAACAATGCTATGATGAGGAGGA
ATGTACCTAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAGAAACAGCTTTTGCAT
ATTCAATCCAGGCATAGGGCGACTATTTAGCACTCAACGATTTTAAAGCTTGTGTATTGC
TGACATAAATTCGGCTTTAGAATCCAATATTGAAAAACGTGAGTACGCAGAGGAGATAG
AAGAAAAGTAGGAAGTTACCGTTTATATTGATTTGTGAAATGCATACTCCGTTGGATGTG
GGGCAACATAGATTTAAGTGTGGATGAAAATTATGTGCTCATTGTGAAAAAAAGTTTGT
CTTTTACTAACAAATTTTTTTTATTATTTGTTTTCAATAGACGTTTCCTCTGACAGAAGAA
AGGCCAGAAAGGCTTATTTCACTGCTCCATCCTCTGAACGTCGTGTTTTGTTATCTGCTC
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGAGACG
ATGAAGTCTTGGTTGTTCTGTTTCCAAGAAGGGTCAAGAAGGTAAGATTTCATCTGTTT
ACAGATTGAAGTTTGCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCACCGGTGCTT
CCGTTCCAATTAACCTTGCACCCATCCAAGCTTGTTATCACTAAGTTACACTTGGACAAGG
ACAGAAAGGCTTTGATCCAAAGAAAGGGTGGTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGIKALPIRRDDEVLV
VRGSKKGQEGKISSVYRLKFAVQVDKVTKEKVN GASVPINLHPSKLVITKLHLDKDRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTATTTTGTGAAAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT
TGCCGCTGGTGCCATATCTTGGTTGCTTGTA CTGCGACCGCTACTACTGTTATGTTGAT
TTTCCGCATTTTCCCCACCGACTAAAACATCCCTTTTGAAGAAACCAATAAGTTGTCCC
AATAGCATTCGAAAATCTTACGCTTTTCTTAACTAGACTTGCCAAACTACTGCTATTCT
TCTTATATCGGCCAACTTGCAAAAACCTCCAATTTGAATCTTCCTACCAATCTCAGCGAAA
TTTTCTTCACTACGATCTCATTTTTCACTGAAATCACTAAGTTTCCTGATAAAGGTATAG
ACGACAGTTCCAACGGTGACCCTTGGATCAAAATTATGTCCTTGTA CGGGGAGTTTATTC
TAATATCAAAAATAACTTATTTCTCTCTCTTTCTTCTGCTCTGAATGCCACCGCTGCTAG
ATAGCGAACTAAGTGAAAACATGGTCTTGCTTCACCTATTTCTCGCCGAGAGCTGTACAA
GATATTTTTTACTTTTGCCATCTTATACTCATCTAATCATCTGTTTCATTTTCTTCTA
TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCGAAGAACTGCCTTTTAA
GAATTGTAAAAGACGAAGTGAAGTATTCAGGAGTATATTATTACATACATACAAAGCAAG
ACAAAGAAACATTTTGTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCTTATAATA
AGAAAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYFLLLPSYTHPNHLFHFP SIFSSSSSSSSSSSFRNRNCLFRIVKDEV
KYSGVYYYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVG VIRPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCTTATAATAAGA
AAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAAATGTCA
TCTTGTATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCTAGTGCGTCTAGTGT
CGATTTTTTTTTTTCACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTGTC
CAATGTCATATCTACAACTCTATACGAAAGTAAACGCACCTTCATTTTTTTGCCCTAAA
ACGGCAATATTTAGACATATCATAAGGGGCCCAAGGGAGAATCGTTAATTTTAAACTTTT

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CTTTGCTCTTGAATGAAAAAGTAAATAAAATAAACTAAATCAAAAAAAGAACGCCACGT
TTGAATTTTAAAGCAAAAATTTTGTGATTAGTAATGATATAAAATAAAACCAAGTCGTT
GGTAAGAATTTGGTTAGGTTATGAATAGTAATGAACTGGATCTAAGAAATAAATATTTTT
ATGAGATATTCGGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG
GCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATGAGGATGAAGATA
GTACTGAAGATGAAAATAAGGCTTCATTGAAGGATTATACACTAGGGCACGACACCGGTG
CACGGTATAGGATAGCACCGGACTGTTCTTCCCACCAATTAAAGGCATCTCCTGTCTTAC
ATATTTCAACAAACCTTAATTCAAGTCCACAATCCTTCACAGGCGATCAGATTTACCTA
CTAATAAAAAAATTTCAATAAATGATTGACCAGACAAGATAAAGGTAACAGTTGCACTA
CCACTTCATCACCTTCTCAAAAAAGATCGAATGTTTTGCTTCCTCACGTAAGAAAACATT
CATCTCCTTCACTATTATCATTTTTCCAAAAACAGTGGCAGTCATATGGGGGATCCAAACC
AGCTATCTACGCCTCCAACCTCCCAAAAGTGCAGGTCACACGATGGAGTTACACAGTTCAT
TCAATGGAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA
CCCAAAATAGACGCTCATCAAACTCTTCCAATCATTCTAGTCAATATCGACGCCATACTA
ATCAACACCAACGTCATCATTCAAGGTCCAAATCAAGTCCTGTCTCTCTGACGGAAATAT
CCATGATCAAAGGCACGCCTTTGGTTTATCCTGCACTTTTATCACTAATAGCAATTAAT
TCAAAACAGACCATCAAATTGAGCACGCATAAAAAGATGGGGTTACTTTACAGAGATTCCT
TTACAGGAAAACAAGCAATTGATACTTTATGCTTGATCATAGGAAGCTTAGATCGTAATT
TGGGCATGTTGATCGGAAAATCGCTGGAAGCTCAAAAATTTGTTCCATGACGTACTTTATG
ACCATGGCGTAAGAGATTCTGTACTGGAGATTTACGAGTTATCTTCAGAATCAATTTTTA
TGGCACATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT
CAGTTAATTCGCTCCGTACTAAAACTGAAATATATGGTGTTTTTGTCCCATTGACACATT
GTTATTCCTCTACATGCTCTCTGAAAAACTTTGCTACTCTATTCTTGCCCCAATCGTT
TGCAACAACAGGCTAATTTACATTTAAAATTAGGTGGTGGTCTTAAGAGAAATATTTCTG
TAGCACTCGATAAGGAGGATGATGAACGAATTTCTTGGACAAATCTGTACCAAAGAGCG
TATGGGAATCATTATCCAAACAACAAATCAAAAGGCAGGAGGCAATATATGAGTTGTTTA
CTACAGAAAAGAAGTTTGTAAAATCTTTGGAAATCATCCGAGATACTTTTCATGAAGAAAT
TATTAGAAACGAATATTATTCCATCTGATGTAAGGATAAATTTTGTAAAGCACGTTTTCG
CACATATCAATGAAATATATTCTGTCAATAGAGAATTTTTGAAGGCTTTAGCACAAAGGC
AATCATTAAGCCCAATTTGTCTCTGGAATTGCAGATATATTTTTGCAGTATCTTCTTTCT
TTGATCCTTTTCTGTACATACATAGCATCAAGACCATAACGCAAGATCTAATTGAAACCC
AAAGATCAATTAAATCCCAATTTTGCTCGTTTTTGACGATGAAGTGTCTAATTCTTCCCTGA
GGCATGGGATCGATTCAATTCCTATCTCAGGGTGTTCAGACCTGGTAGATATTCACGTG
TGGTAAGAGAAATAATACACTTCTCGGACCCAGTAACAGACAAAGATGATCTACAAATGC
TAATGAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG
CAGCACAAAGATCGTTATGACGTTAAAGTGTTAAAGCAGAAAATTCATTCAAAAATGAAT
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAATCAAGCATGAAGGTTTACTCTCAA
GGAAGGACGTGAACAAAACAGATGCGTCCTTTTCAGGAGACATTCAATTTTACCTACTCG
ACAATATGCTATTATTCTTGAAATCAAAAGCTGTAAACAAGTGGCACCAACACACTGTAT
TTCAGAGACCAATTCACCTCCCTTTACTGTTTATTTGTCCGGCTGAGGATATGCCACCCA
TAAAAAGATATGTGACAGAAAACCCAAATTGCTCAGCGGGTGTGCTCTTACCCCAATATC
AAACGAGCAATCCCAAGAATGCTATTGTATTGCGCTATTACGGTACGAAACAACATATC
AAGTTACTTTGTACGCGCCGACGCCGGCCGATTACAGACATTAATAGAAAAGGTGAAAC
AAGAGCAAAAAAGGCTCCTTGATGAAACTAAACATATTACTTTTAAGCAAAATGGTAGGTC
AATTCTTTCACTCATACTAAATACTAATCGCGTCAACGATGTCCTAATCTGTCTATGCTG
GTAATAATTTTATTGGTTGCAACAAATATGGGACTCTTTGTTCTTAATTATGCTACATCGA
TCAATCAAAAACCAAGTGCACCTTCTGCACAAAATATCAATTTACAGATCTCTGTATTGG
AAGAATATAAAGTTATGATTCTTCTAATTGACAAAAAAGTACGGCTGTCTTTAGACG
TAATCGACGATGCAGAAAATGCAGATTTTCTTTTCAGAAAAAATCTAAAGTGTTATTTA
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAAGAATCATTATGATTGCAC
ATCATTTTTTGCACGCCGCACAATTATTGATTGTTAATCCTTTGATATTTGATTTTAATA
GCGGTAATTTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC
CTCTGTCTTTTCTTTTTTGGAGAATAAGATCTGCATTGGTTGTAAAAAAAATATCAAAA
TATTAAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAAATGAGGGAGCTTTTAAATC
TACATGATAACAAAGTTTTAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT
TTCCGATAAAAAATCAACTTTTGCATGTTTTCCAGAACTCTGCTTTTTTCTCAATAAGC

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AAGGGAAGAGGGAGGAGACAAAGGGATGTTTTTCATTGGGAGGGGGAACCAGAACAGTTTCG
CGTGTTCCTACCCTTATATTGTGGCAATTAATAGTAACTTTATTGAAATTAGACATATAG
AAAATGGAGAACTTGTCCGCTGTGTACTTGGAAACAAGATACGTATGTTAAATCATATG
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTGAAATTATCGAACTGTTAA
ATTTTTGA

>YGR070W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRSDTSTPTQLFSGSKVQTNINEISITNDEDEDSTEDENK
ASLKDYTLGHDTGARYRIAPDCSSHQLKASPVLHISTNLNSSPQSFTGDQISPTNKKISI
NDSTRQDKGNSCTTTSSPSQKRSNVLLPHVRKHSSPSLLSFSKNSGSHMGDPNQLSTPPT
PKSAGHTMELHSSFNKGHSSSSSTSSLFALES�KTQNRSSNSSNHSSQYRRHTNQHQHH
SRKSSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSHKKMGLLYRDSFTGKQAI
DTLCLIIIGSLDRNLGMLIGKSLEAQKLFHDVLYDHGVRDSVLEIYELSSSIFMAHQSQS
STSIANTFSSSSSVNSLRTKTEIYGVFVPLTHCYSSSTCSLEKLCYSISCPNRLQQQANL
HLKLGGLKRNISLALDKEDDERISWTNSVPKSVWESLSKQQIKRQEIYELFTTEKKFV
KSLEIIRDFTFMKKLLETNIIPSDVRINFVKHVFHINEIYSVNREFLKALAQRQSLSPIC
PGIADIFLQYLPFFDPFLSYIASRPYAKYLIETQRSVNPNFARFDDEVSNSSLRHGIDSF
LSQGVSRPGRYSLLVREIIHFSDPVTDKDDLQMLMKVQDLLKDLMKRIDRASGAAQDRYD
VKVLKQKILFKNEYVNLGLNNEKRKIKHEGLLSRKDVNKTDAFSGDIQFYLLDNMLLFL
KSAVNKWHQHTVFQRPILPLLFICPAEDMPPIKRYVTENPNCSAGVLLPQYQTSNPKN
AIVFAYYGTKQQYQVTLYAPQAPAGLQTLIEKVQEQKRLLDETKHITFKQMVGGQFFHSYI
NTNRVNDVLICHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVM
LLIDKKLYGCPDVIDDAENADFLFRKNSKVLFKYVAMFKDGFNGKRIIMIAHFLHAA
QLLIVNPLIFDFNSGNFKNLKAGLVDFSVDSEPLSFSFLENKICIGCKKNIKILNVPEV
CDKNGFKMRELLNLHDNKVLNMYKETFKVVSMPFIKNSTFACFPCLCFFLNKQKGREET
KGCFFHWEGEPEQFACSYPIVAINSNFIEIRHIENGELVRCVLGNKIRMLKSYAKKILYC
YEDPQGFIEIELLNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCTACGATTCTCAAGAATCCAGAAGTTTGGCATATT
ATGTATAAAGGCGATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAACC
CGGCCAGTCTGCGCTGCATGCTGTGAAGCAGTAATATGCGATATATACCACATATATTCC
GCTTCCGTTCCAGGATTTTCGAAAAGAGAAACTTCAGTGAAATGACTATGACTACATATTTGG
AGTCTTAGACCATTTGCAAATGAGTTATTCAAGTATGAGAGATCAACACTGATGAGAATAA
ACTCGTCTTCATGATGATACGGGTAACGCGAATGTATCGCATCAATAAATTTTCAGGGAAA
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGTATATAATATTAAGCAGAAAAGAAG
AGGAAAAAATAAATCGGTAAACCAACCATCAACGGTACGAACTTACATTCAAAATCA
ATAATTTACTTTAGAAAAGAATGTCTAATTCTGCCAACTTATCGATGTCATCACCAAGG
TGGCGTTGCCCATTTGGTATAATTGCTAGCGGGATTTCAGTACTCCATGTATGATGTGAAGG
GTGGTTCTCGTGGTGTTATTTTCGACAGAATCAATGGTGTAAAGCAACAGGTTGTGGGTG
AAGGCACTCATTTCTTGGTGCCTTGGCTACAGAAGGCGATCATATACGATGTGAGGACGA
AACCAGAGAGCATTTGCTACCAATACTGGTACGAAGGATTTGCAAATGGTGTCAATTGACCT
TGAGAGTCTTACATAGACCAGAGGTCTTACAGCTACCCGCAATATACCAAAATTTGGGTC
TCGATTACGACGAAAGAGTGTTACCATCTATCGGCAATGAGGTTTTAAAGTCTATAGTAG
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTATTTCTCAAAAAATCAGAA
AAGAGCTTTCTACGAGGGCCAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC
ATATGACGTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGAAGCAGATTGCACAGCAAG
ATGCCGAAAGAGCCAAATTCCTTGTCGAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA
TCAGAGCTGAAGGTGAAGCAGAAAGTGCTGAATTCATTTCAAAGCCTTAGCTAAAGTTG
GTGATGGTCTGTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG
CAAACCTCATCTAACGTTGTCTATTTACCAAGTCAACATTCCTGGTGGTGGTAACAGCGAGT
CTTCGGGATCACCAATTCCTTGCTTTTGAACATTGGCCGTTAA

>YGR132C, 287 aa (SEQ ID NO 178)

MSNSAKLIDVITKVALPIGIIASGIQYSMDVKGSGRVIFDRINGVKQQVVGEGTHFLV
PWLQKAIYDVRTKPKSIATNTGTKDLQMVSLTLRVLHRPEVLQLPAIYQNLGLDYDERV

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LPSIGNEVLKSIVAQFDAAELITQREIISQKIRKELSTRANEFGIKLEDVSITHMTFGPE
FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAESAEFISKALAKVGDGLLLI
RRLEASKDIAQTLANSSNVVYLPSQHSGGGNSSESSGSPNSLLLNI

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAACTGAATCTGAAATTGTTAAACCTGTTCCCTCAAAGCCTGCAAACAAAGACGA
TAGTTCCCTTATTAACACGTTGCGTAGTTTATCGCTGATTACTCCTTCGACACCCAGGT
GAACCTCCAGGAAGAAGGGTGGTGTCTACGATGGTAAGATTTTGCCATTGCCAAAGC
CGATAAGCCTATCCCACTTCATGAATATATAACACTCGCAGAGCTCGATGTTGGAGACAG
TGAGTGAGCAGTGAATTGCTCATGTTTCTCTGCATCCTCATTTAATGACAATTAGCCAT
GTAATAACATCTTGAGGCAGTTAAATATTCGTTACCCTGCAGGTGGCAAAAAATTTATAG
AATAAAAGCATAAAAAGATGGATATCTATGTAATAAGGAAACATTGGCAGAGCGAAGAGA
ACAGACTGCTTTCTATAAAAAGTTTTCGATCAGTCTCTATTTTAATAATTGATTATTGGA
TATAGTTAGTAGTGTTAAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTTCT
CCCCTGAGGGACGCTATATCAGGTTGAATACGCGCTAGAATCCATTTACATGCAGGTA
CCGCAATTGGGATTATGGCATCTGATGGGATTGTTCTTGACAGCAGAACGCAAAAGTCACAA
GTACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAACGATAAAAATTG
CGGTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTCTAATAAATACGGCTAGAATTC
ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCAGTAGAAATTTTGGTGAGAA
GGCTAAGTGATATAAAACAAGGTTACACGCAACATGGTGGTTTAAGACCATTTGGTGTGT
CCTTTATCTACGCCGTTATGACGATAGATACGGTTACCAATTGTATACATCTAATCCAT
CGGGAACCTATACAGGGTGGAAGGCTATTAGTGTTGGCGCTAACACATCAGCAGCACAAA
CCCTACTTCAAATGGACTACAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT
TAAAAACGTTATCCAAAACCTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAATTTG
CTACTATCAGAAAGGTGCTAATGACGGAGAACTGTATCAGAAGATTTTCAAGCCTCAAG
AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAAGGATGAAGACGAAGAAGCTG
ATGAAGATATGAAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGSRRYDSRTTIFSPGRLYQVEYALESHAGTAIGIMASDGIVLAAERKVTSTLLEQD
TSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQ
GYTQHGGRLRPFVGSFIYAGYDDRYGYQLYTSNPSGNYTGWKALSVGANTSAAQTLQMDY
KDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILV
KTGITKKDEDEEDEDMDK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCTCTGATTCATTTGGTGGCCATTACATTTTCCCTCAATGACACA
TTCCCTTATTTTCATAACTGATTAATAATGGTAATGGCACGTGATAGTAGTGGCTCACAAAA
CAAAATTTTCTTTCTCAGCGCTGACAAAGCTTCATTTGCATTCTAACCTTATCACAAACAA
CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCTGACTGATAAATGCTATATCCG
GCATATGCAGTCCACACGGCATTACCGTTTCACTAATTTATTGCCATCTTCCTCCACAGT
TTTGCACCGAAAGGAAAAAAGAAACCAACACCGAAAATTTTTTCTCTAAAGGTTAAA
GTAAACGCAAGGCACCTTACCAGGCTTGTATATATAAATGTCGTGATGCTTCTATGCCAA
AGTAAAAGGCAACACTTGAAGATTTGTTGTAGGCCACTTGCTCAAAGGACATCTAGATA
AATACGACGTAAGAATAAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAACG
TTATCGACTTAGTTGGTAACACCCCATTTGATCGCACTGAAAAAATTGCCTAAGGCTTTGG
GTATCAAACCACAAATTTATGCTAAGCTGGAACATACAATCCAGGTGGTTCATCAAAG
ACAGAATTGCCAAGTCTATGGTGGAGAAGCTGAAGCTTCCGGTAGAATTCATCCTTCCA
GATCTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATCGGCG
CCATCAAAGGTTACAGAACTATCATCACCTTGCCGGAATAATGTCTAACGAGAAAGTTT
CTGTCTTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAAGTCTGCTGCTGGGATT
CTCCAGAATCACATATTGGTGTGCTAAGAAGTTGGAAAAAGAGATTCCTGGTGTGTTA
TACTTGACCAATATAACAATATGATGAACCCAGAAGCTCATTTTGGTACTGGTCGCG
AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTG
GTGCTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAATGATA
AGATCCAAATCGTTGGTGTGCTGACCCATTGCGTTCAATTTTAGCCCAACCTGAAAACCTTGA

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ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG
TTTTGGACAGAAAATTAATTGATGTTTGGTATAAGACAGACGACAAGCCTTCTTTCAAAT
ACGCCAGACAAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTTCTTCCGGTTCTGCCT
TCACTGCGGTTGTGAAATACTGTGAAGACCACCTGAACTGACTGAAGATGATGTCATTG
TTGCCATATTCCCAGATTCCATCAGGTTCGTACCTAACCAAATTCGTGATGACGAATGGT
TGAAAAAGAACAATTTGTGGGATGATGACGTGTTGGCCCGTTTTGACTCTTCAAAGCTGG
AGGCTTCGACGACAAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACT
TGAAACCGGTTGTTTCCGTAAAGGAAACCGCTAAGGTCACCTGATGTTATCAAGATATTAA
AAGACAATGGCTTTGACCAATTGCCTGTGTTGACTGAAGACGGCAAGTTGTCTGGTTTAG
TTACTCTCTCTGAGCTTCTAAGAAAATCAATCAATAATTCAAACAACGACAACACTA
TAAAGGTTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCTCTTACA
ACGAAAATAAATCCGGTAAGAAGAAGTTATTAAATTCGATGAAAACCTCAAAGCTATCTG
ACTTGAATCGTTTCTTTGAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAAACCAA
TCCATATCGTTACTAAGATGGATTTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRHNVIDLVGNTPLIALKKLPKALGIKPQIYAKLELYNPGGSIKDRIAKSM
VEEAEASGRIHPSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG
AEIIRTPTAAAWDSPESHIGVAKKLEKEIPGAVILDQYNNMMNPEAHYFGTGREIQRQLE
DLNLFNLRVAVAGAGTGGTISGISKYLKEQNDKIQIVGADPFGSILAQPENLNKTDITD
YKVEGIGYDFVPQVLDRLIDVWYKTDDKPSFKYARQLISNEGVLVGGSSGSAFTAVVKY
CEDHPELTEDDVIVAIFPDSIRSULTKFVDDEWLKKNLWDDDLARFDSKLEASTTKY
ADVFGNATVKDLHLKPVSVKETAKVTDVIKILKDNQFDQLPVLTEDGKLSGLVTLSELL
RKLSINNSNNDNTIKGKYLDKFLNNFNDVSSYNENKSGKKKFIKFDENSKLSDLNRFEE
KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTTTGGAGGGGCAACGGCGGGTGCACCTTGACTTTCACCTTAAGTT
GTCGTGAAAACCTTCATTTTACCTTCTGGAGTATTCATGGCCTTTGAACGACCAGATTC
CAATTCATATGAGTTGGATGAATTGGATTCTCTGAGGAGATATTAGATCGGGAGTTGAATT
CATGATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAGGTGG
GGAAAGAACATGAGACCCAGATGGAATTGATTATGGGGACATTGTTGCCTTTATATATA
ATTTCAATATACTAATTCAAATGATTAAAAAACGTGAGGGGGACACGCAACTTCGGGTGTT
AAGAAATATTTTGTCTACATTAGATAATGGTGGAGTTTCCTGGCTTGTCGATAAAAAGCCA
TCAAATGTTCGCAGCAGCTCATGTTTACGTTTGTCTTCTGCCCACGTCATATGAGTGG
TATTCTTCTATCAGCACTTGATGAATATTCTTTTCTCATATATCTGAAAGACAAAAGAT
CGGCACGGCAATGCCCTGCAGCATTCTTTCCTAGTTTTTCCGAATTTCCATTACGTATTG
GATCTTGTGCGCATATTTGTGAGTCTTTCACGGAAAAAAGAGCACTGGGTCACCTT
CGGAAAAACCTTTGACTCAATGCAACAGTGTGATAATCCTTTGCGCTGTCTCTTTGAAGA
AAAATCAGGAGTGCAAGATATCGATTAATTCCTTGAAGTTATGATGGTTAGTCTTAGTT
TAACTCTCTTGAAGAAGGGTTTTTTCAGTTGGTCAACACTCTTTAGAGGTAAAAAAGAG
AAAAAAGAGAGAAATTCTTCATGTAATTTACCATGATTCTACGTTTTTGAAG
CAAAAATGAAGATAATCCGAGCGCATGCGAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MNILFLIYLKDKRSARQCPAFLPSFSEFPLRIGSCAHCQSFTTEKKKEHWVTSEKLLTQ
CNSVIIICAVSLKKNQECKISINSLEVMMVSLSLTLKKGFFSWSTLFRGKKKKKKKKR
ILHVIYHDSFLLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAAAATAAGCAAAAAATAAATAAAAAACAAAAACAAAAACAAAAACAAAAAC
AAAAACAAAAACAAAAACACATATTGTTATGATGACTGGACGAAAGAAAGATCGTCGTTA
CTTTCCCTAATTGTTTGTCTTCAGTACAGTTATTATCAGTGTCTCTTTCTTTTATTGT
ACTATGTGATGTTACTGATACATCACGCGCTTCCTTTATGTTTTCTTTTTTATGTTCTGT
TACAGGATTTATAGTTTTTACAGTATATTGACTTCAATAATTTCTAATATTCAGTTCCTA
TAAAAATTGATTATTCCGATTAGATCGGTCGGCGCTACCAAAAAGAGGCGAAGAAAGAG

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GAAAACGCAAGTGGATAAAGGGGTGGGGGGCAAAAGTATTTAAGAAAAAGCGATGCGATG
GAGAGAACAAATGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG
TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCATTAGCATAT
TCTCCATGGCACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCCAAGACGGATA
ATATGGCTACGGACCAGAATAGCATTATTGAAGATGTCAAAAAATATGTGGTGGACATAG
GGGGTAAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTACCTGATA
GCGACCAAATTTTGGACGGTCTGAAAGAACGTTTGAGCTATATTGAAAGCGAGTACGGTG
CTAAATGCAATTTGGAAAAGGATTGAGAAGTTCATGCTCTAAACCGTGACCATTTAGTTG
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLFISIFSMAQASSLSSYIVTFPKTDNMATDQNSIIEDVKYVVDIGGKITHE
YSLIKGFTVLDLPDSQILDGLKERLSYIESEYGAKCNLEKDSEVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTACGTAATGAACTTCCGTAATGAACTTCCGTAATTCAGATCTCTTAGCATCTC
TTGTTCAATCTTCAGACTCTACTAAGTGTCTTACCAACCATTGGATGCTCATTACAAAT
GAATGAATATATTGCACGGAACGGAAGCGGCATGCTTTTTCCGTCCTGCTGTGCTTAGTAA
AGCAAAACGGAGTAGAATCGGTAAGAACTTCTTTTTGGGTGGAAAATCATTGCCATTG
TTTGGACACCTTTCTTTTTCCGTATTGTTTCGAGCACCGCGTTCTTTTTGGGTACTTGAT
GAGGTAGCAGATTCCCTGGAACGTGCTTTCTCTCGAGGTAACCTGCCTTGTTCTCTCTGGT
GACTTTCTAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACTT
TATTTCTTATGTTAAACGGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG
ACGATAATATAGTATCGATAATGCCATTTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG
ACACCAACTTATTCAAACCAATCAAATTTGGTAACAATGAACTTCTACACCGTGCTGTCA
TTCTCTCATTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG
CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA
CCTTTCCCTCTCCACAATCTGGGGGTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC
AAATTAAAGAAATGGACCAAGATTTTCAAGGCTATTCATGAGAATAAATCGTTCGCATGGG
TCCAATTATGGGTTCCTAGGTTGGGCTGCTTTCCAGACACCCCTTGCTAGGGATGGTTGC
GTTACGACTCCGCTTCTGACAACGTGTATATGAATGCAGAACAAGAAGAAAAGGCTTAAGA
AGGCTAACCAACCCACAACACAGTATAACAAAGGATGAAATTAAGCAATACGTCAAAGAAT
ACGTCCAAGCTGCCAAAACTCCATTGCTGCTGGTGCCGATGGTGTGAAATCCACAGCG
CTAACGGTTACTTGTTGAACCAGTTCTTGGACCCACACTCCAATAACAGAACCGATGAGT
ATGGTGGATCCATCGAAAACAGAGCCCGTTTCACCTTGGAAGTGGTTGATGCAGTTGTCTG
ATGCTATTGGCCCTGAAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA
TGTCTGGTGGTGTGTAACCGGTATTGTTGCTCAATATGCTTATGTCTTAGGTGAAC TAG
AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTCTGCTCCATCTAGTTGAACCTCGTGCA
CCAACCCATTTTTAACTGAAGGTGAAGGTGAATACAATGGAGGTAGCAACAAATTTGCTT
ATTCTATCTGGAAGGGCCCAATTATTAGAGCTGGTAACCTTGTCTGCAACCCAGAAGTTG
TCAGAGAAGAGGTGAAGGATCCTAGAACATTGATCGGTTACGGTAGATTTTTTATCTCTA
ATCCAGATTTGGTTGATCGTTTGAAAAAGGGTTACCATTAAACAAATATGACAGAGACA
CTTTCTACAAAATGTCAGCTGAGGGATACATTGACTACCCTACGTACGAAGAAGCTCTAA
AACTCGGTTGGGACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)

MPFVKDFKQPALGDTNLFKPIKIGNNELHRAVIPPLTRMRAQHPGNI PN RDWAVEYYAQ
RAQRPGTLLIITEGTFPSPQSGGYDNAPGIWSEEQIKWTKIFKAIHENKSFQVQLWVLG
WAAFPDPTLARDGLRYSASDNVYMNAEQEEKAKKANNPQHSITKDEIKQYVKEYVQAAKN
SIAAGADGVEIHSANGYLLNQFLDPHSNNRTDEYGGSIENRARFTLEVVDVAVDAIGPEK
VGLRLSPYGVFNMSGGAETGIVAQYAYVLGELERRAKAGKRLAFVHLVEPRVTNPFLTE
GEGEYNGGSNKFAYSIIWKGPIIRAGNFALHPEVVREEVKDPRTLIGYGRFFISNPDLVDR
LEKGLPLNKYDRDTFYKMSAEGYIDYPTYEEALKLGWDKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)

TGGGAGTCTTTAGCAAGTTCGGCAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

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TTTATTCCATTTACTGTCGTTTATACTGGCTGACCCTTAATTCCCTAGCAATCTTTGCCT
GCACCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTGTAGCATAGTTAATA
AGTGCTATTGTTTTTTCATAATGTCACGTGCACTATCAATAATATTACACTCTTGTTCTTG
CCAAATATACACAAAATGCCACATTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG
GACAGCGCTCAGATTAATTGTGGGCTAGATTCTTCACGCTGGAAACGAGTCACCGTTATG
AAAAC TAATGGAATCTCCAGGTTTAATACATAAGAAGGTTACGAGCTACTACATTA AAA
AATACTTTGTCTGTTTTAGCTGTAGATTATTGTAACATTAAAAAGTAACAAACACTGATT
TCGGGTATTTCCCTCCCTAACATGTCTTATTACAGCTGCCGATAATTTACAAGATTCATTCC
AACGTGCCATGAAC TTTCTGGCTCTCCTGGTGCAGTCTCAACCTCACC AACTCAGTCAT
TTATGAACACACTACCTCGTCTGTGAAGCATTACAAAGCAACCAAAGGCTTTAAACCTT
TTTCTACTGGTGACATGAATATTCTACTGTTGGAAAATGTCAATGCAACTGCAATCAAAA
TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCCACAAGTCTTCTCTACCTGAGGATGAAT
TGATTGAAAAAATCAAAGACGTACACGCTATCGGTATAAGATCCAAAAC TAGATTGACTG
AAAAAATACTACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA
ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTCGCCATTCT
CCAATTC AAGATCCGTAGCAGAATTGGTAATTGGTGAGATCATTAGTTTAGCAAGACAAT
TAGGTGATAGATCCATTGAACTGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT
GGGAAGTAAGAGGAAAAACTCTCGGTATTATTGGGTATGGTCACATTGGTTCGCAATTAT
CAGTTCTTGCAGAAGCTATGGGCCTGCATGTGCTATACTATGATATCGTGACAATTATGG
CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG
TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAATTCCG
CTGCTATGAAGGACGGGGCTTATGTTATTAATGCCCTCAAGAGGTACTGTCTGGACATTC
CATCTCTGATCCAAGCCGTCAAGGCCAACAAAATTGCAGGTGCTGCTTTAGATGTTTATC
CACATGAACCAGCTAAGAACGGTGAAGGTTCA TTTAACGATGAAC TTAACAGCTGGACTT
CTGAGTTGGTTTCATTACCAAATATAATCCTGACACCACATATTGGTGGCTCTACAGAAG
AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG
GTAAC TCTGTCTGTTCTGTGAAC TTTCCAGAAAGTCAGTTTGAAGTCTTTGGACTACGATC
AAGAGAACACAGTACGTGTCTTGTATATT CATCGTAACGTTCTCTGGTGT TTTGAAGACCG
TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTTTTCTGATTCTCACGGCGAGA
TCGCTTATCTAATGGCAGACATCTCTCTGTTAATCAAAGTGAAATCAAGGATATATATG
AAAAGTTGAACCAAAC TTTCTGCCAAAGTTTCCATCAGGTTATTATACTAA

>YIL074C, 469 aa (SEQ ID NO 220)

MSYSAADNLQDSFQRAMNFSGSPGAVSTSP TQSFMTNLPRRVSITKQPKALKPFSTGDMN
ILLLENVNATAIKIFKDQGYQVEFHKSSLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA
RNLVCIGCFICIGNQVDLKYAASKGIAVFN SPFSNSRSVAELVIGEIIISLARQLGDRSIE
LHTGTWNKVAARCEVRGKTLGIIGYGHIGSQLSVLAEAMGLHVLVYDIVTIMALGTARQ
VSTLDEL LNKSDFVTLHVPATPETEKMLSAPQFAAMKDGAYVINASRGTVVDIPSLIQAV
KANKIAGAALDVYPHEPAKNGEGSFNDELNSW TSELVSLPNIILTPHIGGSTEEAQSSIG
IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGLKTVNDILSD
HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSAKVSIRLLY

>YIR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCCATGCTTTTGCCGATTTCCTCCACCAACGCTTCCATTGAGACCTGTCCGTGA
TGTCGAGGACACGATAGACAAAATTTGTCTGCACCGTATTCTCTTTGCAAAGACTGCAGAC
CAGCTTCCGTTCTTGCTACGCCGTAGACGATGCATT CATCGTCCTCTTCGATAACAGTTT
TCACCAATTGCAGGCCAATCCCACGGGAGGCACCTGTAATCAAAATAACCTTGCCCATAT
CCCTTCTTTGACAGATTATAAGTTGTTTCTCTTGTGCTGTTTCGCGACAGCCCTTATTTTC
CTGTATTCTTCTCTTTTCTGCATTATCGTTTTTAGCCACTTTACGAAAAAGGTCAAAA
AAGTGAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG
CAATAGTAATAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAAGCTGTCATCTC
GTAAAGTATTCAAGTTTATCATGTCAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG
GCCAACCATTCCCCTTCGACCAATTAAAGGGAAAAGTGGTGCTTATCGTTAATGTTGCCT
CCAAATGTGGATTCACTCCTCAATACAAAGAACTAGAGGCCTTGTAACAAACGTTATAAGG
ACGAAGGATTTACCATCATCGGGTTC CATGCAACCAGTTTGGCCACCAAGAACCTGGCT
CTGATGAAGAAATTGCCCAGTTCTGCCAACTGAAC TATGGCGTGACTTTCCCCATTATGA

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AAAAAATTGACGTTAATGGTGGCAATGAGGACCCTGTTTACAAGTTTTTGAAGAGCCAAA
AATCCGGTATGTTGGGCTTGAGAGGTATCAAATGGAATTTTGAAAAATCTTAGTCGATA
AAAAGGGTAAAGTGTACGAAAGATACTCTTCACTAACCAAACCTTCTTCGTTGTCCGAAA
CCATCGAAGAACTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKGQFFPDQLKGKVVLLIVNVASKCGFTPQYKELEALYKRYKDEGFTII
GFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIMKKIDVNGGNEDPVYKFLKSQKSGMLGL
RGIKWNFEKFLVDKKGVYERYSSLTKPSSLSETIEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAAGTCTGGCGCGCTATTCCTTGCACAATTTTCATATCTTCCCATATGAATACCTG
TTAGTCCGTATCACCAGTGTAACTGTTCTTTACAATGAGAACATCTAGAGTCTTTCTG
ATATGCGTAACTTCTGCCTCATTAATTTAAAAATTTCTTCATAGTAAATAGCTTATTTGC
TTGGAGCAGATGATCGACATGTATTTTTAGGAACATAAACTGCCTAAATATAATAGATCA
GCCTAAAAATAAGAATGCCAATCAACAAAGTTGTATTTCTATCTTCCGATATTTCGCAGT
CCACCATTACAGACCTCTGGTGAGATAGTTTGCCTGCTTTTGCTCCCTTCCAAAGTGCTGA
TAAAAACCTCCGTGATTTTTTGAATACTCCCCTGAATGTCTATTTTAAGTATATTATAAA
ATTAGTTTAAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT
CATAGAGTTCTTTTCATTCATATGCTATACACAAGGTTGTTACGTCACAACTCACAATTCA
CCAAGTTTTCAGGCACATCGCCCAATCTTGGCTCAAAAACCTTTATTTTCGAAGGGTAATT
TGTAAGTACTAGTCTTTTAGTGACAACACTGTATGGGACAGGTCTGGCATGCCTATATCTAG
AATCAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG
ACATTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAGCCAGCACTTGATACCT
ATCAAGAGAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAGTACTTCATTCTTTGA
CGTACAGTGATGTCTCTCAATTTTCGATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC
TAATAGGCAATTCCACCTTAGGCAAAAATCCATTCTTTATAAGGGAAGTGTGCTTAGTG
TTTTAGGGTTCCCACCGTTGATTTATATGGCACTTAACTTAGGATGAAACAGCTGGAAA
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLLRHNSQFTKFSGTSPLNGSKPLFSKGNLYTSLLVTTLYGTGLACLYLESNSLNK
SKEQEDPHAIAEDDIVNIVHDAFNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSVDSQ
FSIVWGFLIQLSSLIGNSTLGKKSILYKGSVSVVLGFPPLIYMALKLRMKQLEKAGVRFE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GTATATTCAAGAAGATGACACACCAAAGCCAAAGCCATTAAAGTAGATGATGAACAATG
GGACTACAAAATGAAATAAAGAAAAAATAGAAATAGGCTAGAAGATCAATTATTAATCGC
CCTATTCTTCTTATTACCTACACAAAATAAAGCAGCAACATAAGAAACAAAAACAAAAT
GAAAACAAACCAAATAAATCTATGTAAGCATACTCATTTCAATTTGATATTCATTACTTG
ACTTTTTTGTCTTATTTGAGGCTCCATAAGCGCGCCATTTTCCCTACTCCCTTTTTTC
GTAAATAGTAATAATGTGCTGAAAAGAACAATGAAGTAGTTATCATAATATTCGTCGT
GTCGATATGAGGGGAGGTGTCTCTTTCTTTCATCCCTTGTCGCAACCTCCAATATATAAG
AGCATAAGCAACTGATCTTACTTTAGTAATTAAGTATGATACCTAGCCCGAAGGAAGAA
AAAAAATTCACCTCAACAACATGGTTCCTAAGTTTACAAACTTTCAAACGGCTTCAAAA
TCCCAAGCATTGCTTTGGGAACCTACGATATTCCAAGATCGCAAACAGCCGAAATTGTGT
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTGATACTGCTGTTCTTTATGGTAATGAGA
AGGAAGTTGGCGATGGTATCATTAAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG
AGGAAATCTTCTACACTACTAAATTATGGAATTCGCAAAACGGATATAAAGAGCTAAAG
CTGCCATTTCGCAATGTTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA
TTCATTTCGCCACTGGAAGGTTCTAAATTAAGGTTGGAACTTGGCGCGCCATGCAAGAAG
CGGTTGATGAAGGATTGGTTAAGTCTATAGGGGTTTCCAACATATGGGAAAAAGCACATTG
ATGAACCTTTTGAAGTGGCCAGAACTGAAGCACAAGCCAGTGGTCAACCAAATCGAGATAT
CACCTTGGATTATGAGACAAGAATTAGCAGATTACTGTAAATCTAAAGGTCTCGTCGTCG
AAGCCTTTGCCCATTTGTGTCACGGCTACAAAATGACTAATCCAGATTTATTAAGGTTT
GCAAGAGAGTGGACCGTAATCCAGGTCAAGTTTGTATTCGTTGGTCTTTACAACACGGTT

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ATTTACCACTACCGAAGACTAAAACCTGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATGAGCCTA
CCGATTGGGAATGCACAGACGCGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI
IKWLNEPDGNHKREEIFYTTKLWNSQNGYKRAKAAIRQCLNEVSGLQYIDLILLIHSPL
SKLRLETWRAMQEAVDEGLVKSIGVSNYKKHIDELLNWPELKHKPVVNQIEISPWIMRQ
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDRNPGQVLIRWSLQHGYPPLPKT
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTACATATCAAAAAGAAGTTATGGCTTATGTGCTCTTTCTAAGTTTGA
CTTTATGCCAAAAATTTCTCCGTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAAGT
GCGCCATAAAAACCTAGATAGAAAAGAAGGGAGAGAACATAAACGCAGAACACCACTACT
TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGAACG
TCTTTTACCTCCTCGATACGTACTGCTTATGCCCTGAACAATTTACATGTAACCCGCAGC
TGCATGCTATATCACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCTCTGGCGCA
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTATT
CGTTCATTGCAACGCTCCTTTCTGCTATCCTTTCGCAAAGTGGCAAGTACTGAAAACCGA
GAAGAATAAATAATATTGCGATGAGTTTATACTTTACGACATTATTTTTATTGCTCACTG
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTGCCCTTGCCATTCCGGATCCGTAGGGGTA
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAAATAAAAACCTATAATCTTTATAA
CGGGTTGCTTGTGGCCTGTTGTTTATTGATTCATGGAAAAGGTCTCAAATTCGTGTTT
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACCTCAAATACAGG
CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTTCAATTTGTACT
TTTCTATCTGTATCCCAACTGTCATGTCTATTGTCAAGAGACTGGTGAATACCAAGGCT
TAATCAACGAACAAGAAAAGCAAAAATTGAACAAACCTTCCTCAAACAGCAAGAAAGACT
CAAATGAAGCTGATTCCACCAAACCTCAAGAGGAACTAAGGAAAAGCAAATTTCTCTGG
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVEVVMLFIFVLPLPFRIRRGIFSTYNQLTAKQQIKTIIFITGCLVGL
LFIDSWKRSQIRVSLYHNDNSGSIGSSAVTPPIQALASRAYNQRMNMYISGFILYFSICIPT
VMSIVKRLVKYQGLINEQEKQKLNKPSSNSKKDSNEADSTKLQEELRKKQISLEGLQKQV
KNLEKYFDEKNQPGNVAAAEASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCTATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAAGATCCCCA
TTATAAAGCCCGCTGTTTTTCTGATTGGAGTTCCTACCGAACTGAGGGGAGGACGCCA
TGAGACGCTCTGTTTGGTGTGCGCATAACCCCTTGCCACTTGAATTGACGGCCTGTTTC
TGCACGCATTCCTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA
TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCACAATTTTCAAGCATTATATGTTTTTAA
CCAAAATTCGGCTCCTTTTCCCTTTTTTCTTATTGGGTGGCGTGCCGTACAGAACGATT
GGCTTGGTGTGAAATCAAGAGCAAGCACAATAGATATCAACATGAACAATATACAAAAGT
CTCTGGCACAGTTTGAAGTTCGTTAGACCAGGCTAGGGCATTCTGAAGCTTTACGTATCA
CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGTATTTGCTCTGGAGGAG
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTGTACAAATTTGGTTTCTTTGAAAGGT
CTAGTGTGGCCAGTTTATGACTTTTTTGGCTGAAACGGTTCGCTTCTAGAACTGGTGCAG
GACAAAGACAAAGTATAGAAGAAGCAACTATATTGGCCACGTTTATGCCAGGAGTGAGG
GCATATGTGGTGTGTTTGATCACCGACAAAGAAATATCCTGTGACAGCAGCATACACACTAT
TAAACAAAATATTGGATGAATATTTAGTCGCACATCCTAAGGAAGAGTGGGCAGATGTGA
CTGAGACCAATGATGCATTGAAAAATGAAGCAACTGGACACTTACATTAGCAAAATATCAAG
ATCCTTCACAGGCTGACGCTATCATGAAAGTTCAACAAGAACTGGATGAGACGAAAATCG
TTTTGCACAAAACGATTGAGAATGTTTTACAAAGAGGTGAAAAGTTGGATAATTTGGTGG

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ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTATAAGCAAGCTAAAAAATCCA
ATTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIYYIGVFRSGGEKALELSEVKDLSQGFFFERSVQGFMFFAETVASRTGAGQRQSIE
EGNYIGHVYARSEGICGVLTIDKEYPVRPAYTLLNKILDEYLVHPKEEWADVTTETNDAL
KMKQLDITYISKYQDPSQADAIMKVQQELDETKIVLHKTIENVLQRGEKLDNLVDKSESLT
ASSKMFYKQAKSNSCCIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCCTGCATTCTGTCAAGAAGGGTATGTGTATGAACATGCAAAT
GACACTGTAAAATGATTTCATTACCCTGATTATGGAGTGATTTTCTTTCTTTTCTTTT
ACATTTAGTTTTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTGA
ATTA AAAAGTGTTACAGAGGAAACCGACGCAAAAAGGCTTGGTGACGCAAACTTTTCCATC
TTTATTTACACTCTTCAGACGGTCCTAAGACCTTTTGAACGTATCAATATAGTTTATCA
TCTGTTCTCTGTTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTACACCCC
TATTTATTTGTCTTAGCGTCCAACCCCTCTCAACCCCTTTCCATTTCTTGTATAAAAGGTA
GTTAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC
CTGCGCAAGATAAATAAGAAATGTCGAAACAGTGGGCGAGTGGTACAAACGGAGCTTTCA
AAAGACAGGTTTCGTCCTTCAGAGAAACAATCTCTAAGCAACACCCAATTTATAAGCCAG
CAAAGGGAAGATATTGGTTGTATGTTTCACTTGCATGCCCATGGGCCCATAGAACACTAA
TTACGAGGGCTTTGAAGGGATTAACCTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC
TTGACGAGAAAGGATGGAGATTTTGGACATGGAAAAGCAATTGGAGGACAGTGAAGATT
TTTTGGAACATTGGCACGATGTTGCAGGTGGTATTAGAACTGCTAAAGAGGATTCCAGCA
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTCATGGTTGATGCTACCAATGAGC
CTCACTATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCCTCAATACTCGG
CAAGGTTCAACCGTCCCAGTCCCTGTGGGACTTAGAAACCCAAACAATTGTTAACAACGAAA
GTAGCGAAATTTATAAGGATTTTGAACCTCTAGTGCGTTTCGATGAATTTGTTCGACGACGATC
ACAAGAAACACGGACCTTGTTCCTGCTCAGTTGAAAACACAGATCGATGACTTCAATTCTT
GGGTTTACGACGATCAACAATGGGTATACAAAGACCGGATTTCGACAGAGAAAGCAGAAG
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGACAAAGTGGAGAAAATCCTGA
GTGACAAATATTCCAAATTGAAGGCCAAATACCGTGAAGAAGATAGACAAAAAATCTTGG
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAGCTGACATTAGATTGTATACTACCG
TCATAAGATTCGATCCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG
CCGGATATCCATTTATTCATTTGTGGGTAAGAAAATTTATACTGGAATTATGATGCCTTCA
GGTACACAACAGATTTTGACCATATCAAGTTACACTACACGCGTTCCACACAAGGATCA
ACCCCTTGGAATTACGCCCTGGGACCCAAGCCAGATATTCGTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETISKQHPIYKPAKGRYWLTVSLACPWAHRTLITRALKG
LTSVIGCSVHWHLDEKGWRFLDMEKQLEDSEDFLEHWHDVAGGIRTAKEDSSKSFAEIK
NDSQRFMVDATNEPHYGYKRISDLYKSDPQYSARFTVPVLWDLETQTIVNNESEIIRI
LNSSAFDEFVDDHKKTDLPVPAQLKTQIDDFNSWVYDSINNGVYKTGFAEKADEVYSEVN
NVFEHLDKVEKILSDKYSLKAKYGEEDRQKILGEFFTVGDQLTEADIRLYTTVIRFDPV
YVQHFKCNFTSIRAGYPFIHLWVRNLYWNYDAFRYTTDFDHIKLHYTRSHTRINPLGITP
LGPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

TCAAGGATACCTGGTTGATTCTACGTCGTCTCTTCACTTTGGTTAATTCACCTTTGCC
TTCACCTTGTGGTGTGCGGGTGTTCAGTCATTAATGTTCTTTATCGCGAGAGGGGTCT
ACATAATCTTGTTTTTTCACTCCAATAAGGCAGTTATAGTGAATTTGTTTTATTACAGAA
GGTGTACCCCTCGTTCGAGTTATTTTACTCTTGTTTTGTAGTTTGTACATCTCTTTATGT
CTGGATCAAAAACGATAATTGCAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC
AACGGGCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTGAACGGGAAGAGGAAAAAAC
CTTCCCATCGCTCGAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAAAAAAATT
CACTTGATGATTGAACTCATCGCACTTTTATACAAAGCAAGAAAGAAACCCAAGTCGACG

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[illegible]

>YKR092C, 406 aa (SEQ ID NO 262)

MASKKIKVDEVPKLSVKEKEIEEKSSSSSSSSSSSSSSSSSSSSSGESSSSSSSS
SSSSSDSSDSSDSSESSSSSSSSSSSSSSSSSDSESSSESDDSSSGSSSSSSSSSDESSSES
ESEDETKKRARESDNEDAKETTKAKTEPESSSSSESSSSGSSSSSESESGSESDDSSSS
SSSSSDSESDSESQSSSSSSSSDSSSDSDSSSSSDSSSDSDSSSSSSSSSSSDSDSDSDS
SSSDSDSSGSSDSSSSSDSSSDESTSSDSDSDSDSDSGSSSELETKEATADESKAETPA
SSNESTPSASSSSSANKLNIPAGTDEIKEGQRKHFSRVDRSKINFEAWELTDNTYKGAAG
TWGEKANENKLGRVRGKDFTKNKNMKMRGSYRGGSITLES GS YKFQD

>YLR043C, 812 bp, CDS: 501-812 (SEQ ID NO 269)

AGACAAGTCTTTCAACGACAACCTCTAAGATCAGAATGATTGAAATCATGTTGCCAGTCTT
CGATGCTCCACAAAACCTTGGTTGAACAAGCTAAGTTGACTGCTGCTACCAACGCTAAGCA
ATAAGCGATTTAATCTCTAATTATTAGTTAAAGTTTTATAAGCATTTTTATGTAACGAAA
AATAAATTGGTTCATATTATTACTGCACTGTCACTTACCATGGAAAGACCAGACAAGAAG
TTGCCGACAGTCTGTTGAATTGGCCTGGTTAGGCTTAAGTCTGGGTCCGCTTCTTTACAA
ATTTGGAGAATTTCTCTTAAACGATATGTATATTCTTTTCGTTGGAAAAGATGTCTTCCA
AAAAAAAAAACCGATGAATTAGTGGAACCAAGGAAAAAAAAAAGAGGTATCCTTGATTAAGG
AACACTGTTTAAACAGTGTGGTTTTCCAAAACCTGAACTGCATTAGTGTAATAGAAGAC
TAGACACCTCGATACAAATAATGGTTACTCAATTCAAACTGCCAGCGAATTTCGACTCTG
CAATTGCTCAAGACAAGCTAGTTGTGCTAGATTTCTACGCCACTTGGTGCGGTCCATGTA
AAATGATTGCTCCAATGATTGAAAAATTCTCTGAACAATACCCACAAGCTGATTTCTATA
AATTGGATGTCGATGAATTGGGTGATGTTGCACAAAAGAATGAAGTTTCCGCTATGCCAA
CTTTGCTTCTATTCAAGAACGGTAAGGAAGTTGCAAAGGTTGTTGGTGCCAACCCAGCGG
CTATTAAGCAAGCCATTGCTGCTAATGCTTAA

>YLR043C, 103 aa (SEQ ID NO 270)

MVTQFKTASEFDSAIAQDKLVVVDYATWCGPCKMIAPMIEKFSEQYPQADFYKLDVDEL
GDVAOKNEVSAMPTLLLLFKNGKEVAKVVGANPAAIKOAIANA

>YLR053C, 827 bp, CDS: 501-827 (SEQ ID NO 271)

AACACTGGGGATATTTGAGATTACCACGTAGTAGATACGGTGGTGTAGATACGTATGAT
TCCATCTTTGAGGGACCAATCCACGATCATGGAACCTTTTAGATAAACGGTGTGCCTATTCA
CCTCCAGTACTGTTTCGATAATGAGGCTAAAGAACGTGATCATGATCGCGATTGTTATCAA
GATTACAATCACGACCACCGGAGTCATTAATATTAAAAAAAAAAATGTGATTGTTAATA

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AGGGGTGGGATGCGCGAAATTCATGCCTACAGTAGAAAAGCGGTTGTTGCACAAATGATT
AAATCTTTATCTCCAACCTACAATACTATCGCGATAGATGCATAATATGTGCAGCTTCTA
AACAGCACGGAGTGATGATAAATACGCATATATGTATATATATATGTATGTGCATATGCA
CGTCCTTTTAAAACTCAAAATACAACATTCTTAGTAAATCCTTTTGTGACACACGTCGG
AACAACTCAGGACGGAGTTAATGGATATGCTTCATAATAAATGTAGTGATGCTATCAAAA
GCACCTCCAATAGCAATTTGAGTAATGAGGTAGACAAACAAAAATTGCAATACGATGACC
TCGGGAACACCGGATTTTCTGAACATTTGAGATGGAATCTCAAGATAATAATGATAGCA
TAGAGGATTTCTTGTCTTTAATATAAATTTAACCCAGGAGTTGAGTTCGAGAACCAAA
GACAATATGAGCACACGAAAAAGACAAAGAAGCATAACCCATTCTATGTACCGTCAGAGG
TAGTGCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

>YLR053C, 108 aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNSNLSNEVDKQKLQYDDLGNLTGFSELFEMESQDNNDSDIEDFLFF
NINLTQEVEFENQRQYEHTKKTKKHNPFPVSEVVREMVKKHALNGRI

>YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)

GTGAAATTGAGACTGATAGGTGAGAGGTGAACCAATTGAGTGAGGAGTGGTTTAGTTACA
AATGCAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG
AATGAGGTCTTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTTCTCTGATTCA
TTCAGGAAGAAAAGGGCGAAGTCCTCGAAATGAAAAATTC AACATCATTAACAGACCGGC
GCGCGCTTTACAATTTAGTATGTACGCCACCAATAAAAGCTGCTTAAACAATAAGCTAG
AAAGCCCAAAGGGTGTTAAATAGTACAGCGAACCCCTCAGCAACGGTACATCAACAACCC
CTTGAAAAGAATAGAGACAATACAGCTACAGTCATCCCCTTCTCTTGTATTTTTGGCCAC
AATTGATTGTATTACATCATATTTTGCCTGTGCGCTTCTTCTATCTTTTCCGCATAAACT
AGGGGAAACCGGATGAAGAAATGGATTGGCTGAAAAATACAACAATTGTAGTGTTATTCA
GTCATTCAACTGACAAAAGTAACAAACACAAGAAACGTCAAGTCCAGTGCAATATGCGAA
AGAACACTTTAGATATGGTCACTATAGGTATCGCATGCCTTGTGGGAGTCTACACGGGCA
CGAGATTTTTCGAGCCCATTGTTATCGATAGATTGCGTAAGGATGGAACTTGAGAACGG
ACATTTCCCATCCCAGAATACGACGAGGACGGAAATCTGTTAAAGGTCACGCCGTCTTTAT
CATCCACACCAGCTGCACCACCTACACCACCTACACCTCCTACTCCACCACAACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)

MDWLKNTTIVVLFSSHSTDKSNKHKRQVQCNMNRKNTLDMVTIGIACLVGVYTGTRFFPEPI
VIDRLRKDGNLRTDIPPIPEYDEDGNLLKVTPSLSSSTPAAPPTPPTPPTPPTPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTTCGTTTCATCTACGAAATGTTGCTGGCATTGGCATCTCCACAA
GATGACATCCCAACGCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAACAACG
AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTCATCCAATATAACGCCCCCTATATG
TATGTACCTTTACCTTTTATTTAAGTACTAGTGCTGTTTAGTTAGGTTATGTGAAGGCAC
GGGTTTGTCTTTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTTCAAGCTTTTAAGCG
CCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTCAGCCTGGACA
GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATTGTGGTTATAGAAC
ATCGCAGCGCCTTTAAATATATTGTCTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA
ACCACGGCAAAGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATTCA
AAAGGCAGTCATCGCCATTACAGAGAAATCATCTCTGCGGATCACCCAATTTATAAACCTG
CTAAGGGAAGGTACTGGCTGTATGTGGCGCTACCATGCCCATGGGCACAAAGAACCTTGA
TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGTAGCGCATTTGGCACC
TGGATGACAAAGGCTGGCGATTCCCTGAAGAAGGAGATGGGAAAACCAATGAAAGGCAC
GGTTTGACATTGCAGGCGGAATTAGCTCAGTAAATTTAAATACCAGTACTCCTGTGGCTA
ACATACCAATAACGCGCATCGGTTGTGTGGTCGACGGAACAGATGAACCGCATTACGGGT
ACAAGAGACTAAGCGACTTCTATTTCAAAACAAAGCCAGACTATAAGGGAAGATTACCGG
TACCTGTTCTTTGGGACTTGGAACATGCACTATAGTAAACAATGAAAGCAGTGATATCA
TCGGAATTATGAATTCCGCTGCGTTTGATGAGTTTGTGCGCGAAGAATACCGTCAAGTCC
GTCTGGTACCTCGGTCTCTAGAGGCACAGATTACAGAGTTCAACTCTTGGGTGTACGATA
AAATCAACAACGGTGTATACAAGGCCGGTTTTGCAGAATGTGCAGAGGTATACGAGAGGG

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AGGTAACAAGCCTTTTTCAATATCTTGACAAATTGGAAAATCTTCTGGACAAGAAGTACA
CAGATTTGGAGGCGGAGTATGGTAAGAACAACAAGGACAAGATACTAGATCGCTACTTTG
CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCAACGATAGTAAGGTTTCG
ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATTATCCCC
GTATACACACGTGGCTCAAGAATATATACTGGCGCCACGAAGCCTTCCAGCGCACAACGG
ACTTTACCCACATAAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)

MSEKSASNNKAEFKRQSSPFREIISADHPIYKPAKGRYWLYVALPCPWAQRTLITRALKG
LAPIIGCSVAHWHLDDKGWRFLEEGDGKTNERHWFDIAGGISSVNLNTSTPVANIPNNAH
RLLVGDGTDEPHYGYKRLSDFYFKTKPDYKGRFTVPVLWDLETCTIVNNESSDIIGIMNSA
AFDEFVGEERYQVRLVPRSLEAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ
YLDKLENLLDKKYTDLEAEYKNNKDKILDYFAIGDTLLEADVRLYPTIVRFDVVYQH
FKCNLATIRDDYSRIHTWLKNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPIGITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC
CTGAAGGATACCTTACAAACTCTGGTAGGAACCTCGGTTATAGAATAACCCTTTAGCCT
TTTTTACGTACTTGTATACCGTTTAAATTTTCCTATGTACTATAACCTTTTTTCACTACT
ATTATGGAATTCTATCGAGCGACCGGGCTTTTGTGTACGGAAGAGTGAAAAATCGAGTTT
TGGTGTTTTGGTGAAAGAAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT
CAATAACAAGTCGTTCTGTGTCAGTGGTATTGAAGTTGTGAGATCTAAGAGTAGAGAGAAG
GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTTAAGGTTTTTATTTGGTCTCCTAGA
ATTTAAGGTCTTAGTTAGTTTTGGTTTTGTGGGTACATATTTTCAATTCAAAGGA
GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTGCGTACTACAT
CAAGCGATAAGGCGATCGCTAGTCAAAGGGATAAACGGAAGTCTGAAGTTTTGATTGCTG
CACAGTCCCTTGACAATGAAATCCGCAGCGTAAAAAACCTAAAAAGATTGTCGATTGGGT
CAATGGATTTACTTATTGATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA
GACGATCATGGTCTGGCACGACATCCAGTTCTGCGTCAATGCCAAGTGACACAACCCCG
TTAATAACACACGATATAGCGATCCAACCTCCGCTAGAGAAGTGCATGGGAGGGGTAAC
CAGGGATAGAATCCTCCAATAAGACTAAACAAGGTAACCTACTTAGGTATAAAAAAGGTG
TTCCTCTCCATCCAGGAAATTAAATGCTAACGTATTAAAGAAAACTTATTATGGGTTT
CCGCCAATCAACACCCCTAACGTTAAGCCTGATAATTTTCCTAGAGCTTGTACAAGATACTT
TACAAAATATACAACCTAAGCGACAATGGTGAAGATAATGATGGGAATAGCAATGAAAATA
ACGATATTGAGGATAATGGGGAGGATAAAGAATCACAATCATATGAAAATAAGGAGAACA
ACACTATCAACTTGAACAGGGGGCTGTCAAGGCATGGAAACGCGTCACCTAATACGAAGGC
CTTCAACATTGCGGAGGTCATATACAGAGTTTGATGATAACGAAGATGACGATAATAAGG
GAGACAGTGCCCTGAAACAGTAAATAAAGTGAAGAAAGAAATCTCCAAAATAAAGAGA
GACCAGTGTCTGTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAAATAGTGCAGGAC
TAACCGACAATGATGCCATTACATTAGCCAGAAGCTTAGTATGGCTGGTTCATATTCAG
ATAAAAAAGATCAACCACAACCGGAAGGGCATTATGATGAAGGAGATATTGGTTTTTCAA
CTTCACAAGCGAATACTTTGGATGATGGTGAATTTGCCCTCAATATGCCCATCAATAATA
CCATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA
GGTCACAAGAGCAAGAAAAAGAAGTAGAACAAAGTGTGGATGAAATGAAAAACGACGACG
AAGAACGTCTAAATTGACCAAGAATACAATAAAGGTCGAAATAGATCCGCACAAATCCC
TTTTTAGACAGCAAGATGAGGATTCTGAGAATATGAGTTCGCCTGGGTCAATTGGTGATT
TTCAAGACATTTATAATCATTACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGAA
TAGAGAAAGAAGCCGAAGAGGTACCCGTCAAGGTTGAAATGACACAGTAGAACAAAGACT
TAGAGTTAAGAGAGGGAACAACAGACATGGTAAAGCCAAGCGCAACGGATGACAACAAG
AAACGAAGCGACATCGTCAAGAAACGGATGGACATGGTTGAACAATAAAATGAGCAGAG
AAGACGATAACGAAGAAACCAAGGGGACGATGAAAATGAAGAAAACGTGGATTACAAA
GAATGGAGCTCGACAATTCCAAAAAACATTATATTTCTCTATTTAATGGCGGTGAGAAGA
CGGAGGTGTCAAATAAAGAAGAAATGAACAATTCAGTACTTCCACCGCCACATCACAGA
CAAGACAGAAAATCGAGAAAACCTTTTGCGAACCTATTCAGAAGAAAGCCACACCACAAGC

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ATGATGCATCATCATCACCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG
ATGCCGTGCACGTTGCGGTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAGGGAGC
CGGTTGAACCCATTGTGTTGCGCAATCGCCCTCGTCCTCACCGTCACCATCACAGCCGTC
ATGGTTCCCAAAAAATAAGCGTAAAAACCTTAAAGATTCTCAGCCGCAGCAGCAGATAC
CATTACAACCACAATTGGAAGGCGCAATAGAGATAGAAAAGAAAGAGGAAAGCGATTCCG
AGAGCTTGCCCCAACTACAGCCGGCCGTTAGTGTAAGTAGTACCAAAAGTAACCTAGAG
ACAGAGAAGAAGAGGAGGCAAAGAAAAAGAACAAGAAGAGGAGCAATACGACAGAAATTT
CCAACCAACAACACTCCAAACACGTCCAAAAGGAGAATACCGATGAGCAAAAAGCTCAAC
TACAAGCTCCAGCTCAAGAACAAGTCCAAACTTCAGTCCCAGTTCAAGCTTCAGCCCCAG
TCCAAAATTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAACCTCAGG
CTCCAGCGGACACCATTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG
CAGACGTCAAAAAACCTGACAAACCAAACTCCCCGGTTCAATTCACAGACAGTGCCTTTG
GGTTCCTCACTGCCCTTGCTGACAGTGTCTACGGTTATCATGTTTCGACCACCGTCTACCAA
TTAACGTCGAAAGGGCCATATACCGGCTGAGTCACTTGAAATTGAGCAATTCGAAGAGGG
GACTGCGCGAGCAGGTATTACTAAGTAACTTCATGTATGCTTATCTGAACTTGGTTAATC
ACACTCTGTACATGGAGCAGGTAGCCACGACAAAGAACAACAACAACAACAACAACA
AACCCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRDNESMLRTTSSDKAIASQRDKRKSEVLIAAQSLDNEIRSVKNLKRLSIGSMDLLID
PELDIKFGGESSGRRSWSGTTSSSASMPSDTTVNTRYSDPTPLENLHGRGNSGIESNN
KTKQGNLYGIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNFLELVQDTLQNIQLS
DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRRS
YTEFDDNEDDDNKGDSASETVNKVEERISKIKERPVSRLDITEELTKISNSAGLTDNDAI
TLARTLSMAGSYSDKKDQPPQEGHYDEGDIGFSTSQANTLDDGEFASNMPINNTMTWPER
SSLRRSRFNTYRIRSQEQEKEVEQSVDEMKNDDERLKLTKNTIKVEIDPHKSPFRQQDE
DSENMSSPGSIGDFQDIYNHYRQSSGEWEQEMGIEKEAEVFPVKVRNDTVEQDLELREGT
TDMVKPSATDDNKETKRHRRRNGWTWLNKMSREDDNEENQGDDENEENVDSQRMELDNS
KKHYISLFNGGEKTEVSNKEEMNNSSTSTATSQTRQKIEKTFANLFRRKPHHKKHDASSP
SSSPSSSPSIPNNDVHVVRVRSKSLGNKSGREPVEPIVLRNRP RP RHHHSHRHSQKIS
VKTLKDSQPQQIPLQPQLEGAIEIEKKEESDSESLPQLQPAVSVSSTKSNSRDREEEEA
KKKNKKRSNTTEISNQQHSKHVQKENTDEQKAQLQAPAEQVQTSVPVQASAPVQNSAPV
QTSAPVEASAQTQAPAAPPLKHTSILPFRKLTADFVKPKDPNSPVQFTDSAFGFPLPLL
TVSTVIMFDHRLPINVERAIYRLSHLKLNSKRGLEQVLLSNFMYAYLNLVNHTLYMEQ
VAHDKEQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAATCAAGAGCATGTA
GATGTTACGGATCGACTCAAAGACCTCTGTCACTCTGAAATTTCTAATAATTATGCACA
CCACGCTAGTATAGATACAGCTTGATTTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA
TCTATGTATAATATAACCAGATAAAAAATACACCTTCGTACAAGGTGCTAATAATGTTGAG
AATTCGAAATTCCTTTTTAAAGGCGTATTCGCTATTGAATGATTGAAAAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATCGCAGAAAAT
TTTTCCTTCAGTTTATTTGTCTTATAAAAAGACTGTCCTACGCTCAAATAACTTATACTT
TTCTGTATCTCATTCAAATTATTTCTTGTCAACAACCTGTAACAGAATTAAGCACTATT
AAGGCAAATTTAGAGCAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA
ACTACAAGTCTAGAGGTGGCGACTTCCGCGGTGGAAGAACTCTGATAGAACTCTTACA
ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTTCGTTCCAATTACAACC
AACCCAGGAATTGATCAAACCAAACCTGGGATGAAGAATTACCCAAATTGCCAACTTTTCG
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCCGCACAGATCGGACAGTGAGATTGCTC
AGTTCAGAAAGGAAAATGAAATGACTATTTCCGGACACGATATTCCAAAGCCAATCACCA
CTTTCGATGAAGCTGGTTTCCCAGACTACGTTTTGAATGAAGTGAAGGCTGAAGGATTTG
ACAAACCAACTGGCATTCAATGTCAGGGTTGGCCAATGGCTTTATCTGGTAGGGACATGG
TTGGTATTGCTGCCACTGGTTCCGGTAAGACTTTGTCTTATTGTTTACCAGGTATTGTTT
ATATCAACGCTCAACCATTATTGGCTCCAGGCGATGGACCAATTGTTTTGGTTTTGGCTC

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CAACTAGAGAATTGGCTGTTCAAATTCAAACAGAATGTTCCAAGTTTGGTCATAGTTCCA
GAATCAGAAATACCTGTGTCTACGGTGGTGTTCAAAAAGTCAACAAATCAGAGATTTAT
CTCGTGGCTCTGAAATTGTTATTGCTACTCCAGGTCGACTAATTGATATGCTAGAGATTG
GTAAGACTAATTTGAAGAGAGTCACCTACCTGGTTCTTGATGAAGCTGATAGAATGTTAG
ATATGGGTTTTGAACCTCAAATCAGAAAGATTGTTGATCAAATCAGACCTGATAGACAAA
CCTTGATGTGGTCTGCCACTTGGCCAAAGGAGGTGAAGCAACTAGCCGCTGATTACTTGA
ATGATCCAATTCAGTTCAGTTGGTTCTCTAGAACTATCTGCCTCCCATAATATTACTC
AGATCGTCGAAGTTGTTTCTGATTTGAAAAGAGAGATCGTTTGAACAAGTACTTAGAAA
CAGCCTCTCAAGACAACGAATACAAGACATTAATCTTTGCTTCTACGAAAAGAATGTGCG
ATGATATCACCAAGTATCTAAGAGAAGATGGATGGCCCGCCTTGGCTATTTCATGGTGACA
AAGACCAAAGAGAACGTGACTGGGTCTACAAGAGTTTAGAAACGGTAGATCCCCAATTA
TGGTTGCTACTGATGTGGCCGCCAGAGGTATCGGTATGTTAAAATTTTCTCCATTTTTTT
ATTGATTTTTATTTTTTTTTTGTACCCTAACGATATTACAGCTATTTCTAATGGCTTTT
AATGACATTAATGACTTTATGACAACCATGATAGTACAGAAGAGAGACCTTTTTTCTTTT
TTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTCTTTTTTTTCTTTTTTTTTTTTTTTT
TCGAATCTAGACTCTATGTGAGTCTATTCTCGATGGGGAGTATCGGAAATTGAATTTTAA
TTCGAATGACTTCTAATGCATCACTACAGAAAACATAATATTGGGAGGATGAGAAAAATTG
ACTTTAATTAGTCGTTTTGAGAGACGGGAAATTATAAACTCGGAGAAGTGTATTGTGTT
CATGATTTGCACTTCATGTCAAAGAAATTTTCGCTTTTTGACATCGGCGCAAATAAACAA
GGAATTTGGCTTTTTCAGCTTATTTCTAGAACGCATACATACGCTTCGTTGATCGTTGTTTT
TTTCAATGCTTGGCATTGTGTACAAGGGTAGATTGTTTTATTGGAATAATAAGTATATT
CTACTTTGAAATGCCGTCATCCTTCTTGACTATTGTTATTCTCATTTTTGTGTAGTTTATG
CATTTTTGTAGTTATATTGAGATACTGTTGCATCCCAAGTTCGAATTATTAAGAAGTGCTG
ATAAAAATGGAAAATAACAAAATAAAAGGATTTCAACCATATTTCAGAAATCATTTACTTT
GTTTTCTCTTTTTTTAAGTGCTAGCTTTCATTTCAGTTTGAATAAGGATTCTGGAGTATTGA
TGATTAAATATTTTGAATTTCTTTAATAAAAAATATAATTTCTGATAATCTTCAAGCCAGGG
GGAAATTTGAGACAATGTTGGGAGTCCAAACATGAATTTGTGGGGGGCATGAAAATAAAG
TTCATATACAGAATAACGAACCAAATTAACAGTATGCTTTGTAAACGTTTGTTTACT
TCTTTATTTTTTTCAGATGTCAAAGGTATCAATTACGTTATCAACTACGATATGCCAGGTA
ACATTGAAGATTATGTTACAGAATCGGTAGAACTGGTAGAGCAGGTGCTACTGGTACTG
CTATATCTTTTCTTCCACCGAACAAAACAAGGTTTAGGTGCTAAATTAATCTCTATCATGA
GAGAAGCTAATCAAAATATTCCTCCCGAATTATTGAAATACGACAGGAGATCTTATGGTG
GCGGTCACCCAAGATACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
GTTACGGTGGTGGCCGTGGTGGTTACGGCGGTAACAGGCAGAGAGATGGTGGCTGGGGTA
ACAGAGGTCGTTCAAACATTTGA

>YNL112W, 546 aa (SEO ID NO 328)

MTYGGRDQQYNKNTNYKSRGGDFRGGNRSDRNSYNDPRPQGGNYRGGFGGGRSNYNQPOELIK
PNWDEELPKLPTFEKNFYVEHESVRDRSDSEIAQFRKENEMTISGHDIPKPIITTFDEAGE
PDYVLNEVKAEGFDKPTGIQCQGWPMALSGRDMVGIAATGSGKTLSYCLPGIVHINAQPL
LAPGDGPIVLVLAPTRELAVQIQTECSKFGHSSRIRNTCVYGGVPKSQQIRDLSRGSEIV
IATPGRLIDMLEIGKTNLKRVTYLVLEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSAT
WPKEVKQLAADYLNDPIQVQVGSLELSASHNITQIVEVVSDFEKRDRNLNKYLETASQDNE
YKTLIFASTKRCDDITKYLREDGWPALAIHGDKDQRERDWVLQEFRNGRSPIMVATDVA
ARGIDVKGINYVINYDMPGNIEDYVHRIGRTGRAGATGTAISFFTEQNKGLGAKLISIMR
EANQNIPELLKYDRRSYGGGGHPRYGGGGRGGGGYGRGGGYGGGGGGYGGNRQRDGGWGN
RGRSNY

>YNL131W, 959 bp, CDS: 501-959 (SEQ ID NO 329)

CAAAAAGAGCTAATCAACTCCTTGAAGCTTAGATAAATACGCCATAAATGATAACAGTGAG
GAATGGGCTGAATCTCAAAAATCTTTAGAAAATAGCTGCCAAGGCCAAAGGCGTCGTCAGT
TAAAAAACTGGTAAAAAGAGAACGACTGAAAAGGCTGAAGATATCTATAGACAAGAGATG
AAAGCTATGAAAAAACCAGAAAGTCTAAAAAGGCTGCAAATTAAGCGTTCTACTCTTTG
TCAACCCTTTTATAGCTAAACGTTTACTTAATTTGTACAATAATATAGAATAGAAACAT
AGTTGATGTTTGAACCTTTACATATTCTTTCAATCGTGTCGAGCGATATAAGTATTACG
ATTATGCCGGCGAAAACCTGAACCCGTTTTAGACAATTTCAATCAACATACTCCACTCCGT

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AGTGAGTAACTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAAGTATATACCC
CCAAAATAAGCATCATTCAAATGGTTCGAATTAAGTAAAGACGATGTCGTTCAAT
TAGACGAACCACAATTTTCCAGAAATCAGGCCATCGTGGAAAGAAAAGGCTTCTGCAACAA
ACAACGACGTTGTCGATGATGAAGATGACTCTGATAGTGATTTTGAAGATGAATTTGATG
AAAATGAAACATTGTTGGACAGAATCGTTGCTTTAAAAGACATTGTCCCCCAGGTAAGA
GACAAACAATTTCTAATTTTGGTTTTACTAGCTCTTTTGTGAGAAATGCTTTACACAA
AATCCGGAACCTTGCTTGGACTTTGACCACCCTGCTTTGTTACTCGGTGTGCCACTAT
CCTTATCTATACTTGCCGAACAACAGCTAATCGAAATGGAAGACATTTGATTTACAAA
GTGATGCTAATAACATATTGGCCCCAAGGTGAAAAAGATGCTGCAGCAACAGCCAATTAA

>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNDVVDDEDDSDSDFEDEFDENETLLD
RIVALKDIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTTALLLGVPVLSLSILAE
QQLIEMEKTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAAATACACACGGCGGAAGCCATCATCGAGGCCCAAAGCAAGGATAAAGCATGCTTTTT
CCTGGATAAACAGAAATATAATAAACCGATACCTGGGACCATAATCCACACACCTGCTGA
AGCCACACCGATCCATCCCATGTTGGCCAAGTCAAATTGTGTATTCAAATCTGTTGTCAA
CGAGTTACCACCCGTTCCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA
TATTGTATTGTAATATATTAAGTATGATATATTACAAAACCTAACTTCTTTCAAAGCTCT
GTGCAGACTTATTATTTAAGAAGGATATTTAATTTGAAAGGACGTGAAAGCACGAATGAT
TACTACCCACTGATGTTTGGTTAGCACATGTGTAACCTACTGCTTATATATGGTGCAGAAA
AGTGGCTCGGAATGAACACCTCTTGTAAGTGAATCTTATTGATAAGGCACAGGCTCTTC
ACGCCGCTTAGTATTTCGTCGATGCGTGAGCAATTGAAGCTTTTTACGAGGGAAATAGTCG
ATTTTACATTCTTATCTTATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA
ACAGCAGTAAGAAGAGACCGAAGGATTCCTTCTTTGTTATCGGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAGAGATGCTTATCTTATCTTCTTATCTTAAAGACCTACCATTTGTT
CTTTTCTATTTTGGCAGCCCGGTATTTCGAAAGGGAAAAAAAAACCAAGACAGCATTCCT
TGTTCAATTATGACTATTACAAAGCCAGGAATGATTTTCGATGCGCGACATGAATTACGTCG
TTTCCAAGAACAGAAGCTTAAACCGTCCTGCTGAGCGGGCGGTAATCGGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQLKLFTR EIVDFTLILSGFDYYQTL L I S S N S S K R P K D S S L L S E K K K K K K K K K D V
L S Y L S Y L K D L P F V P F L W Q P G Y S Q R E K N P R Q H S L F I M T I T K P G M I S M A D M N Y V V S K N R S L
N R P A E R G G N R

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTTAATTTCAAATACCCTAATCGGAGGTCTTATCTTATTTTTCAAGGGCAAGGC
TCTCCACATCGGTAAGTGATGACCAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC
ATACAAGCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGTGTGCAAAAGTGGTTTTGTTC
CCCGACGCCCGGGCCTTTCTCTCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA
CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAAATTATCCTGCGTGT
TTGCTTCGGTCTTAGCTTTTACTTGGGTATGCGAGAACCTCTAAGAGCTTAGACCGGTCT
TCCTCCCTAAAAAGAAAATTATAAAAGGTTATTATCTGGACTAAAGCAAAAAAAAAACAA
CGTTTCGGCGTCCGCTCAAAATTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG
GTTATGACGAATACGATGAGATGAGTAATTGCAGAAGGCTCCTATGCAGACAGCTAAGCA
GTGCTTACTTGAATTACCTTCCCTTTTATTTCTTGATATATCGTCCTTTTCTCTCTATC
TTAGTTCTTGCGAGTACTGGCAATCATGTTTCTCCTTTTTTTTTCTTTTTTTTTTATTTT
TTTTTTTTTTTTTTTACTTTTTCAGTTTCTCGTAGCTTTTCTTATTTTGCTATTTAAAGTAA
GTTTAAATAGTACCCTCACTAAACACGTACGGCCGATCCACCAACGAACAAAAGCACGAT
CCTTGACCCATCATTTGTATTCCAAAGCGTTGGAACATTCATTTTTTTTTTCCGGTCTAT
TGCACAAGACAATATCCAGAATATTCAGTTGGATAGGAAATACAAGACAGGTGGCACCCA
CAAAGCACACGCCGAAATATTTATTAAATACAATATAG

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>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCFSFFFLFFLFFFFFTF
QFLVAFPILLFKVSLNSTLTKHVRPIHQRTKARSLTHHCIPKRWNIHFFFSGLLHKTI SR
IFSWIGNTRQVAPTKHTPKYLLNTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCATTTCCTACTGCTATTCCCTGTTGCTATTGTCAGAACCATTGTTTACTTGAATGTTA
TTACTACCATTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT
GTATTTTTCGCGAGACGTCTCTCAAATATATGGCCAAAACACCTTGATATTCTAGTTTATTC
CATTCGTCCTTCTTGAAGTCCCATTATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT
TGCTTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAAGCTTTTCTATAGAAT
TCTAACTGTGTGGCAGAGTTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT
TCTTGTGATGTGTGCAAAGATAAATGCTTATCTGAACGTTTCTCTATTGTTTTTTCGTC
AATTTTCTTTTCTTTCTTCTGCTTCGCGTTTTTCGACATATTAAGCTGTATATAGAAGAGAAA
AATGCGCAGAGATGTACTAGATGATAAAAAATAATTGTAATAACGTTAATATATATAAAAT
ATTATCTATTTTCATTTAAAGTTTATATTCTGCCCTCAAATTTTAAAATTTGGGAGGCAG
TGTCGTCAATGGTCTCTTTCAAGTTCCTGAACTTGAAACCTAACAATTTCTTACTCTTTT
TATTATCAAGAGTAGCACCAAGGGTGTTATGGGTAGCACCAGAACCTGGTTTTCCCCACTG
GAATATTGCCTTTTAGAACAGGGAAGTCTTCGTTAAGGATATCGAGAACATCCTGCATAG
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MIKNNCNNVNIYKYLFSEFKVYILPSNFKIWEAVSSMVSEFKFLNLKPNNFLFLLSRVAP
RVLWVAPEPGFPTGILPFRTGKSSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GCGTGAACATATGTCATATTTGCGATTTTAGGTACAATAAATATTATCATTATTATATTAT
GTTTGCATGTAGGTTCTACAAATACATTGTTGTACGCTATAGTTTCCTTTCAAACATAGA
AAGAATTCGTAAACAAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC
AATACCTTCTCATTTCACAATTTGGCCCTCACCTCTTTGTACAAAAAACGTCGCCATTG
ATAAAATAAGTAAGAAGCATATAAATTGGAATTGTCATTACGTAAAAGAAAAAAATCATG
TGTAACATATTACGTAATAGAAATACGGAATTTTCTCGCGGAAGTAGATCTTCCGTGGAAAA
AAAGGAAAAAGTCCGATCAATATTGAAAAAGGGATCCTTAGTTTCCCAACTATATAAGGA
GGAAAAGTCTATCTCTGTAGCGTTGATATAACGTGTACGATTTTCAAACAAACAGATAGC
AGTATCACACGCCCCGTAAATATGTCAGTTTTTCGTTTTCAGGTGCTAACGGGTTTCATTGCCC
AACACATTGTGCGATCTCCTGTTGAAGGAAGACTATAAGGTCATCGGTTCTGCCAGAAGTC
AAGAAAAGGCCGAGAATTTAACGGAGGCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG
TTGTCCCAGACATATCTAAGCTGGACGCATTTGACCATGTTTTCAAAAGCACGGCAAGG
ATATCAAGATAGTTCTACATACGGCCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC
GCGATTTATTAATTCCTGCTGTGAACGGTGTTAAGGGAATTTCTCCACTCAATTAATAAAT
ACGCCGCTGATTCTGTAGAACGTGTAGTTCTCACCTCTTCTTATGCAGCTGTGTTTCGATA
TGGCAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT
GGGAGAGTTGCCAAAGTGACCCAGTTAACGCCCTACTGTGGTTCTAAGAAGTTTGCTGAAA
AAGCAGCTTGGAATTTCTAGAGGAGAATAGAGACTCTGTAAAATTCGAATTAAGTCCG
TTAACCCAGTTTACGTTTTTGGTCCGCAATGTTTGACAAAGATGTGAAAAAACACTTGA
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG
AACTATTTGGTGGATACATTGATGTTTCGTGATGTTGCAAAGGCTCATTAGTGCCTTCC
AAAAGAGGGAAACAATTTGGTCAAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG
ATGTTCTCGATATCCTTAACGAAGACTTCCCTGTTCTAAAAGGCAATATTCCAGTGGGGA
AACCAGTTCTGGTGCTACCCATAACACCCTTGGTGCTACTCTTGATAATAAAAAGAGTA
AGAAATTGTTAGGTTTCAAGTTCAGGAACCTTGAAAGAGACCATTGACGACACTGCCTCCC
AAATTTTAAAATTTGAGGGCAGAATATAA

>YOL151W, 342 aa (SEQ ID NO 352)

MSVFVSGANGFIAQHIVDLLLKEDYKVIQSARSQEKAENLTEAFGNNPKFSMEVVPDISK
LDAFDHVFQKHGKDIKIVLHTASPFCDITDSEKDLIPAVNGVKILHSIKKYAADSVE

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RVVLTSSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAWEFL
EENRDSVKFELTAVNPVYVFGPQMFDDKDVKKHLNLTSCELVNSLMHLSPEDKIPELFGGYI
DVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLIDLNEFPVLKGNIPVGKPGSGAT
HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGCTCAGTACCTACACGCTCCTCTGACATAGAAGATGAT
CCATCTGTGGTTGTTGCAGCAGGTTTCAGAATCTTCCTCCTGGGGCTCAGCAAATGGATTG
TTATCCAGATCATCATATGGATCATAAGGTACAGCCGAAGTCATTGTTTCAGAGGATAGAT
GGATTGACTAAGGGTACAGTACGGCAAAAAAATTAGATCAGCTTTTCAAACAAACTA
TTTTGGCGTTTACCAAACCAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG
TCCCTTTTCTACAAAATTAGGCTTTGAACGCGTGCTATGGAAAAAGTGTAAGAAAACG
AAAAAACAGAAAAGTCATATATATCTTATAACGAAATATCAGGGTGTTTCACTCAATCG
CCAGGTGCCGCTAACACAATCATTAGGATAGTCGGGCAATATATACGGTTCAATAGTCAC
TGAAAGTGATACACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAATAACACATCA
AAGCGGTTGTATTTGATATGGATGGCACATTATGCCTACCCCAGCCTTGATGTTTCCAG
CAATGAGAAACGCCATAGGATTGGAGGACAAATCGATTGATATCCTTCATTTTCATTGATA
CATTGCCCCACAGAAAAGAAAAAAGAAAGCGCATGATAGAATAGAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCGCAGCCTGGTCTGGTTGACATAATGAGGTATTTGACGA
AAAATGGTATTTAGCAAGAACATATGTACTAGAAATGTCGGAGCCCCGGTAGAGACTTTTG
TAAAAAGATTTATTCATCCGAGCTTTTCGAGGTTTGACTATATTGTGACAAGGGAGTTTA
GGCCTACAAAACCGCAACCAGACCCATTATTACACATCGCCTCGAAGCTAAATATAAGGC
CCTTGAAAATGATCATGGTAGGAGATTCAATTTGACGACATGAAATCCGGTAGATCTGCTG
GATGTTTCACGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG
AACTAGTAGACGTTTCAGTAGAGGATCTTCCGAAATAATTGAATTGATTCAAAATATGA
ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

MTKLQGLQGLKHIKAVVFDMDGTLCLPQPMFPAMRNAIGLEDKSIDILHFIDTLPTEKE
KKEAHDRIELVEAKAMKEMQPPGLVDIMRYLTKNGISKNICTRNVGAPVETVVKRFIPS
ELSRFDYIVTREFRPTKPQPDLLHIAASKLNIRPLEMIMVGDSFDDMKSGRSAGCFTVLL
KNHVNGHLLLEHKELVDVSVEDLSEIIELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCACC
CTGACGCATTTGCCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCCAAACCTG
ACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGAGAAAGCTCAAA
AAGTCGCCTCCTCACATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATT
GGGTTTCTCATGGGGTGATAAACTTGACTTATAGCCTTGATACTCTAGGTATGTACCC
TGTGTATTTTCGTAAGCTAGTAACGTATTATGCCATTTATGTACACACCGTTCATAATATT
TGCCTATTGCATTGGCTGTGATAGCGGCGCGCAAAGAAATTAGGAAGTATAAAAAAAAAA
AATACAAAACCTTAATCTGAATGGAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG
ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTCTCTCGAGGACAGTTT
CTGCAAGATCGCCTACATTGGTCCTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA
CTTTTGACCAGGTCAGGAACCTAGTCGAACACCCCAATGATAAAAAACTATTGGTAGATG
TAAGGGAACCCAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATCCGGTGA
ATAGTGCCCCCTGGCGCTCTTGGAATGCCCGAAAAGGAGTTTCACAAAGTTTCCAATTTG
CTAAACCACCTCACGATAAAGAATTGATTTTCTTTGTGCGAAAGGAGTAAGAGCCAAAA
CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCCTGGTTCTA
TTACTGAGTGGTTAGCTAAAGGTGGTGCTGACGTTAAGCCCCAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MFKHSTGILSRTVSARSPTLVLRFTTKAPKIYTFDQVRNLVEHPNDKKLLVDVREPKEV
KDYKMPPTTINIPVNSAPGALGLPEKEFHKVFQFAKPPHDKELIFLCAKGVRKTAEEELAR
SYGYENTGIYPGSITEWLAKGGADVKKPKK

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>YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAGCTCCTACAGTGAAATATCTGGGTGCTACTGACGCCAAGCCCTACAGCGATCGGA
ATGCGGGAACGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG
CAAACAAAAACCCCCAAAATTTCAATTACTTAGAATGACCCCTCAAGAGCAGGGTGCAATTTT
ATCAAGCGATCATTGAACTAACTAAGTTCATATCCTGTATAGGATTTAAAACAATGCACC
CTAAGTTCAAATGCACCCCCCTCGCCCCGAGCGGACCCCTTGAACAGAGAACTGTTTCG
AGGTTACCCCAATTGGATCACCTTGATAATTTGTAATCGAGTTCGGATAAGATGTATACG
AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTACCTAGCAATATATGTATAAAAC
AGGAATGTGTGCGTGCTTCAGGCAGAATTTTACGGTCCCTTGTA AAAAAGTCTATCATAAA
GCCATCACAAAACAATAATAATGAAATTCTCAACTATTTTTCGGAGCTACTACAGTTATGA
CTGCCGTCTCGGCAGCAGCTGTGTCGAGTGTAATGACCACCTAAGACTATTACTGCTACTA
ACGGTAATAACGTTTACACTAAGGTCGTTACCGACACCGCTGACCCTATCATTAGTTACA
GTACCAC TAGAACTGTCGTTGTCAGTAATAGTGATGCTACTTACACAAAGGTTGTCACCG
AAGGACCAGATACCACCTCTGAAAAGAGTACAACAAAGACACTTACTTTGACAAACGGTT
CAGGTTTCATCAACCAACCTTTACACCAAGACCGTCACTCAAGCCGTCGAATCATCTACAT
CTCCTCATCCTCCTCATCCTCCTCCTCCTCTCTCGCCTCTTCTTCTGGTGCTGCTCCTG
CTGCATTCCAAGGAGCAAGTGTGCGGTGCATTGGCCCTTGGTGTGATTTCTTACCTATTAT
AA

>YOR382W, 153 aa (SEO ID NO 376)

MKFSTIFGATTVMTAVSAAAVSSVMTTKTITATNGNNVYTKVVTDTADPIISYSTTRTVV
 VNSDATYTKVVTEGPDTTSEKSTTKTLTLTNGSGSSTNLYTKTVTQAVESSTSSSSSS
 SSSSSASSSSGAAPAAFOGASVGALALGLISYLL

>YPL078C, 1235 bp, CDS: 501-1235 (SEO ID NO 379)

TAAACTGTGTTGTGACGCAACTGCAACTCCAGATGAAATACGGTCCGGTAAAGATAGGA
ATATTCTACTCTACAAGCATGAATATTTTTTAAACGCGGCGCAGTACTATACAGCATAACA
GGTCTTCCACGCATGAGAACTGTCCATGGCTAAATTAGTTCCCTCACACAGAATTAGAAA
TGTGCTGTGACAATGGCACATACGTAGATAAAAAGATAAATATAATTGAGAATGGCTGTGC
CGACAACATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGGCCGGGTAAATCGACA
TCAATATTGAACCAATCACGACGCTTTTTCTCTTCAACGCTCATTCGGACCTTCACCACA
GGTTTGGGTAATTAAAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG
TTTATACTGTGCTAGGAAGGGTTATATTTTATTAAAAGACTGACGAGAATTCAGTACCTC
CTAAGTGCGCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTAGCGTTAAGGT
CCGTTTCTAA AACATTATTTAGCCAAGGTGTTTCGTTGTCTTTCGATGGTGATTGGAGCCC
GTTATATGTCTTCCACTCCAGAAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA
TCAATGCCATTCCAGGTAATAATATTTTGACAAAAGACGGGGGTTTTTGGGGACTTCTGCTG
CCGCTGTCAATTTATGCCATTTCCAATGAATTGTACGTTATCAACGATGAAAGTATTTTAT
TGCTGACTTTTTTGGGTTTCACTGGTTTTAGTGGCAAAGTATTTGGCGCCAGCATATAAAG
ATTTTGCCGATGCAAGAATGAAGAAAGTCTCCGACGTTTTTAAATGCCTCGAGAAACAAGC
ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTGCTGAAA
CTACAAAGGTTTTGTTTGATGTTTTCCAAGGAAACTGTTGAACTTGAAAGCGAAGCCTTTG
AATTGAAACAAAAGGTAGAATTAGCTACGGAACGAAAGCAAGCAGTCTTAGATTCTGTTGGTTA
GATATGAAGCTTCTTCGCGTCAATTGGAACAAAGGCAAGCTAGCAAAATCTGTCTATCTCCA
GAGTTCAGTCAGAATTGGGTAATCCAAAATTCCAAGAGAAAGTTTTGCAACAGTCTATAT
CTGAAATTGAACAATTGCTTTCTAAATTGAAGTAA

>YPL078C, 244 aa (SEQ ID NO 380)

MSMSMGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPAKANSIINAIPGN
NILTGTGVLGTSAAAVIYAI SNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQQLQNVAAETTKVLFVDVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVSQSELGNPKFQEKVLQQSISEIEQLL
SKLK

>YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTGACAGTAAATAATAAAAGGTGAAATGATTAAACAATGA

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AAGCGGCAGAAAAATAAAATCAAACAGTGGCAGTATTGACTTTTGAAAATCAGAAGTTCA
TCCTAAGTTAAGACTTTCTTCTTTTAAGTGCTTTCTCCTTCTCTCACTGTCTTATCGCTG
TATATCTCATTGTTGAATAATATAACACAACGTTATAAGTGATCATCACTTTCTGATCCA
TAATTTCAAACCTCAAGCGACCGTACATGTGGCATTTCCTACTATAAACTTACGAGCAAG
AGAAAGATATACGGAAAAGGTTAATTGGCAGGTTACACAAGATTTTGGTCATTGAATATT
TGCAGCCCTCCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCCTTTTCAAAT
AGTGGTATTTAACTGGCCATAACCAAGGAAACCGTTGTACCTATTATTTTGTATAGTCTT
CATTTAATAACGTGTTAAGAATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAGA
AGTTGAAGCAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC
TTGAATTACCAGAAAGTACGATTAAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG
AATCTGACATAGCTTCAAATCTGATGTTCCCTCCGGTCTCATCATCTACCAATATCTCTC
CGGCTAATGAAACACAACCTAGAAATACCTGATACTCAAGAATTGCATCATAACTGCTCA
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACCTCAATCG
TTGAACATGACTCTGTTATTACCCAAACAAAACAGCCATGTCTCAAGAATACGAAGAGA
CTGCCGCTCACTTATCTTCGAGAAATCCATCGCTCGATGTAGTCGCGGGAGAACTTCACA
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG
AAGAAGAGGGTGAAAATCACGACAGCATAATAATTTTCATCATTAAACGATGCTACCCCTT
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG
GTGATACGCCAACTCACAATGTTCTCTAGGCACAAAAGACAATGAAAATAATGACGATG
AGTATTGTAATGATAAGGAAATTAGTTTGAACGCAAATAATGTGCTTCCTGATGAACTTT
CAAAGGAAGAAGATGAAAGATTAAACCTAGAAACGCATGTATCAACCGAAGAAAAGAAAC
AGGATATCGCTGATCAGGAACTGCAGAAAACCTATTACGTCTAGTACAGAACCATCTG
AGAATAAAATAAGAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG
ATCAGAAGGTTCCATGGGAGGAAGATGTGAAGAAAGATTTTCATAATGAGAACACAAATA
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG
CTTTGAAAAAGTCCGAAAGTTGTACAGCCGCGGACGAGAGGTCGTACTCTGAAGAACTT
CAGAAGATATCTTTCACGGACACGACAAACAGGTAGTTGAAGGCCAAAATGATTTCACTG
GGAAAATATTGAGAATGAAAGCCAGAAATTAATGGGGGAAGGGAATCATAAGTTACCGT
TGTCTGCCGAAGCTGACATTATAGAACCCTGGTAAGGATATTCAAGATCAAGCCGAGGATT
TGTTTACGCAGAGCAGCGGAGACTTGGGAGAAAGTTTGGCCATGGGAATCTACTTGCTTCTG
ACGCTGATGTAAACGAGCAAATCCCAAGAGAAACATGAAGATTATTTGCTGCTTCTGGA
ACGATGAGAAACTTCTTGGGAAGTTTCTGACGGTGAAGTATCATCGGGAAAGACGGAAA
ACAGCATGCAGACTAGTACTGAGAAAATAGCTGAGCAAAAAGTTTTCGTTTTTGGAAAACG
ACGACGACCTTTTGGACGACGACGACAGCTTTTGGCTTCTTCTGAGGAAGAAGACACAG
TACCTAATACCGATAATACAACGAATTTAACCTCAAAAACAGTTGAAGAAAAAAGGCTT
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATGCGTCAAGAGCAAGTTCAATTTTA
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACGGTTTGACTAAAACCTGGACTAG
GCACCCCCAACCAACAAGTCAGTGTAACCAATATAGTTAGTCCTAAGCCTCCTGTGGTAA
AAGACAATCGTTCAAATTTTAAGATAAATGAGGAGAAAAAGAAGTCTGATGCTTACGATT
TTCCACTGGAAATTATTTCAAGAAAGTTCCAAGAAGGGTCACGCAAAGCCGGTTGCCGTTT
CTACTCAAAGGTTTGGCTCAGGGAATTCTTTTAGTTCTTTGGACAAACCAATTCCACAGA
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCGTGATCCCATTTGGGGACGCAGGAGC
CTCGATCTTCGAGAACTAACTCAGCGATCTCGCAATCTCCCGTTAATTATGCTTTCCCTA
ACCCATACAAAATTCAACAACCTACAACAGGCTCCTATCCAATCAGGTATGCCTTTACCAA
ATACCAACATACCTCCCCCAGCATTAAAAGTGGAACCACCGTTTCTGCTCCTCCAATTC
GGGCAAGAGGGGTCAGCAATGCCTCCGTGGGAAGTTCAGCGTCTTTTGGTGCTAGACATG
CAACACAGTACGGCCTCAATAACGGGGTACCTCCGGTTTCGCCATATGGTCAAGCTACCA
TAAATTTGCCAACTGCGAATAAGTATGCCCCGTCTCTCCTACAGTTCAGCAGAAGCAAT
ATCCATCAGTTGTGCAAAACCTTGGCGCTTCGGCCGTAAATACCCCCAATTTTGTAAAGA
CCCATAGAGGCCATACAAGCTCTATTAGTTCTGATACACCAAACCAGAATGAACACGCCCT
CTAGATACGCACCCAACCTATCAACAATCTTATCAGGTGCCATATACCTCACAACCTGTGTG
GTCCTGTAGCTGGGAATTCAAGCTATCAAAGCCAAACCCGAAGTTCTTATGCAGTTCCCTA
TGATGCCCCAGGCTCAAACCTCAGCAAGTATTCAGCCTCACGCGAACATTCAACCGCCTA
CTGGCATTTTACCTTTAGCCCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAACT
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAAATTCACCTACCTCTTGCAAATTTGCCAC
TTGCTGAAAACATACTGCCAGAAATTATCACGCATCGAGCTACAAGTAGTGTGACCAC

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AGCCACGTTTCAGGCCCATCAATAATTCCTACCTCCAGTACATGCCACATCAGTTATTC
CGAACAAATCCAATCACTGGTGAGCCTTTGCCGATCAAAACATCCCCTTCTCCTACAGGAC
CCAATCCAAACAATTCTCCATCACCATCCTCTCCCATATCAAGGATTTCTGGCGTAAACT
TGACTAGCAAAAAGGCAAACGGTTTGGATGATTTATTGAGTTTGGCAGGAGGACCCAAAC
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TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

MTPEAKKRKNQKKKLKQKQKAAEKAASHSEEPLELPSTINSSFNDDSVNRTESDIASK
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TQTKPAMSQYEETAHLSSRNPSLDVVAGELHNNNEHTQKIAVSAVEEDSFNEEEGENH
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ISLNANNVLPDELSKEEDERLKLETHVSTEEKQDIADQETAENLFTSSTEPSENKIRNS
GDDTSMFLQDDESDQKVPWEEDVKKDFHNENTNNTQESAPNTDDRDKGYEGNEALKKSES
CTAADERSYSEETSEDI FGHGDKQVVEGQNDFTGKNIENESQKLMGEGNHKLPLSAEADI
IEPGKDIQDQAE DLFTQSSGDLGEVL PWESTDKNADVTSKSQEKHEDLFAASGNDEKL PW
EVSDGEVSSGKTENSMQTSTEKIAEQKFSFLENDLDDDDSLASSEEDTVPNTDNT
TNLTSKPVEEKASRYKPIIEEEAGMRQEQVHFTNTTGI VTPQQFHGLTKTGLGTPNQV
SVPNIVSPKPPVVKDNRSNFKINEEKKKSDAYDFLEII SESSKKGHAKPVAVPTQRFGS
GNSFSSLDKPI PQSRKGSNNSNRPPVIPLGTQEPSSRTNSAISQSPVNYAFPNPYKIQQ
LQQAPIQSGMPLPNTNIPPPALKVETTVSAPPIRARGVSNASVGSSASFGARHATQYGLN
NGVPPVSPYQATINLPTANKYAPVSPTVQQKQYPSVVQNLGASAVNTPNFVKTHRGHTS
SISSYTPNQNEHASRYAPNYQQSYQVPYTSQFVGPVAGNSSYQSQTRSSYAVPMMPQAQT
SASIOPHANIQPPTGILPLAPLRPLDPLQAATNLQPRASNITAANSLPLANLPLAENILP
EII THRATSSVAPPRQENNP IKIDNEALLRRQFP I FHWSAANKVVYAVPPIPDQSQY MIS
SSIVQEI KVTPIDQII KPNMMLKSFPGPLGSAKLKKDLTKWMETTIKSISENESSTDMT
IWQLLEMKLNDKVNWNK NISKLLYNSDELLMYLSQFFPNGDMI PNAYRLDINCQMRVLAFL
QTGNHDEALRLALSKRDYAIALLVGSMLGKDRWSEVIQKLYEGFTAGPNDQKELAHFLL
LIFQV FVGNSKMAIKSFYTNNETSQWASENWSI VAAVLINI PENNEDPLLI PPVVLEFL
IEFGIFLTKKGLTAAASTLFIIGNVPLSNEPVMADSDVIFESIGNMNTFESILWDEIY EY
IFSYPKFKG FSSILPQKIYHASLLQEQLNSLGTKYTDYLSSSVRKL PKKDILTINLTR
ELSEVASRLSESN TGWLAKPKLSSVWGQLDKSFNKYIGGDDIDALNKKNDKKKVDFGFTP
GSSANSSTVDLTQTFTPFQAQVTSQSYVDTTALLHNAHNVP SHSVLHKS PNVSKGLVEA
NLPTYTHRIGDSLQSPQRIHNTQFAAAEPQMASLRRVRTDQHTNEKALKSQILEKKSTA
YTPQFGQNH SVPMKSN SNVPSLFADFPAPPKLGTVP SNYVSSPDLVRRESII STGSEFL
PPPKIGVPTKANSSQGSMLYSPSVEALPIDPVVPQVHETGYNDFGNKHSQKSMPEDESHT
SHDNSNADQNTLKD SADVTDETMDIEGPGFNDVKNLLPMEPNHQPTSTVNPIQITISDDIQ
PILQTNVEVRGTDASKMENS LPSIENERSSEEQPENISKSASSAYLPSTGGLSLENRPLT
QDENS ISETVQSTYLPAGSISMEAKPISQVQDVPRNVN KASKLVEQHMAPPKPKSTDAT
KMNYSPYVPQSTAASADGDESTILKTSPAIYARTHQA HASNPSQYFPLVNQANETASFEL
SESTSQAQSNGNVASENRFSPIKKA EVVEKDTFQPTIRKASTNQYRAF KPLES DADKYND
VIEDESDDDNMSTDEAKNRKEEKKNVNMKKETKPSNKDIDDKSNGWFGWLKKDTGDKKVY
KAKLGHKNTLYYDEKLKRWNKDATEEEKQKII ESSAPPPPPIVKRKDGGPKTKPRSGPI
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>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

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GAAAAAGCGCTATTCTTATTTCGCTTCCTAACTACCGCCCTAGTTCGTGCTTGCATTTTTT
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AAAATGAAGCGGAAGAAGCAAAGGACAAAAACAATTCATTTGATTTTGCCACTTCTAAA
TGAAGGTCTAATAAAAGCTATCTTGAGCATCTTTATTAGATTCTGCACAGCAACAAGCGA
TTTTCTTTGGTCAAAATATAATAATTGACTTACGTTTTTCCCGGACTGTCCTTTCATAAT
ATAATAACCATCTGCAAGCCATGTCTAGATGAAAACCATAACAGTGATGTTCAAGATATTC

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CTTCACCTGAACATATCCGTCGATAGTAACCTCTAACGAGAATGAATTGATGAATAACTCAA
GCGCAGACGATGGAATCGAATTTGACGCCCCAGAGGAAGAAAGAGAAGCCGAAAGGGAGG
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CTCAAAGCGTTAGAGATGCAATTGAATGCGAGTCTCAAGAAATGAACCTTTGGCAAAAAAGT
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GCAACATTTTCGTTAAAGAACCGCAGATCGTACGTATGCCATTGAGGTTTTCAACAGGT
TTAGGGACGGGACTGGTTTGGAACTGATATGATTTTCTTGAACCAAGAATGGAACCTGG
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GAAATAATTCTCGTCTACTGATTACCGTGCTATGAGCCATCAGCAAAACATATATGGCG
CTCCTCCTCTCCTGTTCCAAACGGCCAGCTGTTCGGACCTCCTCCTCAAACAACTATT
ACCAGGGTTACAGTATGCCTCCTCCACAACAACAGCAACAGCCATATGGTAATTATG
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AGAGCTACGGTCGCTACCAGACTTCTATTCCACCACCACCTCCACAACAACAAATTCCTC
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CTATGAACTCATCCTCTCCCCCTCCTATGAGTACCAATTACAATGGTCAAAATATATCTG
CAAAACCTCTGCCCCACCAATGTACACCAACCTCCGCCACCTCAACAACAACAACAAC
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TAGATAGTTTAGCAAACTACAAAAATAG

>YPL190C, 802 aa (SEQ ID NO 388)

MSDENHNSDVQDIPSPELSVDSNSNENELMNNSSADDGIEFDAPEEEREAEEREENEEOH
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DDDDDDDEEEEEEEEEEGNDNSSVGSDSAEDGEDEEDKKDKTKDKEVELRRETLEKEQK
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ILAMLNSNSDTALSVPPHDSITSTASASATSGARSNDQRKPLSDAQRMRFPADLSK
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NIKNAFGFIQFDNPQSVRDAIECESQEMNFGKKLILEVSSSNARPQFDHGDHGTNSSSTF
ISSAKRPFQTESGDMYNDNGAGYKKSRRHTVSCNIFVKRTADRTYAIEVFNRFRDGTGL
ETDMIFLKPMELGKLINDAAYNGVWGVVLVNKTHNVDVQTFYKGSQGETKFDEYISISA
DDAVAIFNNIKNNRNSRPTDYRAMSHQQNIYGAPPLPVPNGPAVGPPPQNTNYQGYSM
PPQQQQQQPYGNYGMPPPSHDQGYGSQPPIPMNQSYGRYQTSIPPPPPQQQIQGYGRYQ
AGPPPQPPSQTTPMDQQQLLSAIQNLPPNVVSNLLSMAQQQQQQPHAQQQLVGLIQSMQGG
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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

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ATTGGTTGGACAACGTTGATGTTACCTTCCTTGTTATGGAACCATCCATCATTTTCTAGT
TCTTCTTCTGCAATATTGCCTTTTGGGAAGAAGGATCGAAAGTAGCCATTTGCAGACACG
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TTGCAGCTCAACCCCGCATTTCCGGAGTTTCTTTTTTTTTTTATTTGGGGTAATTTGGAGG
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TACATGTGTATAAGCGAAATCACAAGGATAATAATGTATTGCTAAACACCCTCAAGAAAG
AAAATAATCATAACGAAATCATGGGTATACCTATGCAAATATACCAGGATGGGAAGGGGG
TGCAATTTTACCACACGAGATATCAGAACGTATTTGACGAACGGGCGAGCAAGTATGGCA
ACTACACGGTGAATAATGATTACCCACAGCTTCCAGATACGATAAAGGAACATATCGACC
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ACGATGATGGTGACGAAGAAAAGGAACTTGAAGATGTTTTTCGAAGTAACCGTGGGTTGG
AATTTGTACGGATTAATAACTATTTTACTACCCACGATTTACAAAGTTTCAAAAAGTTTTA
GAAATTTCAATAGCAAGTACTGGATTTTTTATTCTAATCAAGCAGAGGACAAAAAATTAC
TGCTGTATGACTTTAACGGCCAACATTTGATTTTTTATTAAGCAGCAATTTTACGGGCAGT
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ACACCATTCAAATTTTAGTTGGATTTTCAAGATGGAAAGTTGTTAAAGCTAAACTGCGACT
TGAACGGAAACGTAAACAATCACTTGCTTTTGAAGGATCCTTCAACTTCCTCTCATCAAA
GCCACCTATCTATATTAAATGTCTGGGCAGGTTTGTGGCCACATTTTCGTTGTTCTTTTA
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CCAACATGAGATATCTGTCCATTCCAACAAGAGACCCCATAGAGAATTCAAATTTCTCTC
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ACATTCAAACAATTCTTCTTAAATAA

>YPL201C, 461 aa (SEQ ID NO 390)

MGIPMQIYQDQGVQFYHTRYQNVFDERASKYGNVTVNNDYPQLPDTIKEHIDQLTFSNV
GEDGGDVGNYSSEDDDGDEEKELEDVFRSNRGLFVRINNYFTTHDLQSFKSFNFNSKY
WIFYSNQAEDKLLLYDFNGQHLIFIKQQFYGQLNLLLSDAIICMDCNFGYNSNTIQILV
GFQNGKLLKLNCDLNGNVNHLKDPSTSSHQSHLSILNVWAGLLPHFVVSFSLKDGLL
ITSLDHQQSNGSFQSFHTNIDLVDLRTTTNVKSVLNFQFTLYKGNDMIFHCKNLLGSD
ASTLNKEINFMLKIDEDVQKIDYLLKTNHILLETNMRYLSIPTRDPIENSNSPPVSDSE
VYPIFYKTQELHVASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD
IRAKYGIRSVKDLFVGNCPSVNSPVLITLTDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2:
685-1176 (SEQ ID NO 393)

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GTTGCATAGATAGGATGGGTGAGCGCAATTACTAGTTACGCAGTAAGTAGGTTATATGGC
TGCTGGAGGGGAGTACTGATTTAATCACAATCCGGATTAACTTCCTCCTGAAAAAAA
AAACTACATCAAGTCAAAGATTTTCATTCACTCTTTGGAAGGCTGTGTGGCATTCTAA
CCTTTATTTTTTTATCACCATTCCTCGAATTTTCGTGGTTCGCTTTCTTAGCGCCGTTATT
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CTTGTTATTCCGAAAGAAAGATCTAAATTTGCAATTGGTAGTGAAAACAAATAAACAAA
GACATAACCGCACTCCAATCATGTCCGAATATGCATCTAGTATTCATCTCAAATGAAAC
AATTCGATACCGTATGTAAGATGGTTTTATTGGTTCATCGTCATCATGGTTCAAACAGC

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CAAATGACCCGACACACGTAACCGAAGCAGTTATACTAACAAGAAAGCTAATTTTCACCC
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AATAAACTAATTTGCCTAAATCTTATTTAGTTGCTGGTTTAGGTTTCGCTTATCTCCTT
TTGATTTTTATTAAACGTCGGAGGTGTAGGTGAAATTCCTTCCAATTTTGCTGGGTTGTG
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CTCTTGACCTACTGGATTGTCTTTTCATTTTGTAGTGTCAATTGAATTCTGGTCCAAGGCA
ATTCTATATTTGATTCCATTCTACTGGTTTTTGAAAACCGTTTTCTTAATCTACATTGCC
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GAGGCTTCTAAGGCTACAGGTGCTTCTGTTTCATTAA

>YPR028W, 180 aa (SEQ ID NO 394)

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YDR145W, 2120 bp, CDS: 501-2120 (SEQ ID NO 99)

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AAAACGATGTGTATGAATCCCGTCTTAATTAGTAAATAGGGTCTAGTAAG
CGTAGCGAGGATGAATTAAATGCATTGTTGAATATGAAGAGCACCTTATG
GTATATAAATGTACAATCTTGATTGATGACAGCTTTGCAAGTAAACGTAT
CAAATGAATATCACGATTTTGGCTGTATTACCCGGGCAGTATACGCGGCG
AATTTTGTTAAAAAATGTGTTAGACTTAAGTCGGAGCAAATGAATAATGG
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GCATTGCAATCATAACCGAATCTTTGCCAGTGTGTGTATAAAATACGACA
ATGCTTTCCAATCCAGAAAATCTGGTGTTAATGCCAATAATAATACGGG
CACTGGTAACGCTGATGCGATCACAGGAGCTCAGCAAAATATGGTACTGC
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GAAGACAACAGGCTGCGCAAGCCTACAATAATACTTCAAATTCAAATTCA
AGCAATCCAGCTTCTATTCTACTGAAAATGTCCCTAATTCATCACAGCA
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CGGACGAAGGGCCCAAGCAGCAGCTACAAGAAAAGAAAATTGAACTGCTT
AACGATTGGAAGGTGCTAAAAATGAGTATACCAAGCTGTTCAATAATTA
TCAAAACAGTAAAAAACATTCTATGTAGAGTGTGCAAGACACAATCCGG
CTTTACATAAATTCTTGCAAGAAAGCACTCAACAGCAACGAGTGCAGCAA
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AAATCGGCAATATTCAAACAACAGAGCCTGCCATACCCATATCGGAAAA
TATATCTACCAAAACACCAGCACCGGTAGCTTATAGATCCAACAGACCTA
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ACAATAAATTACCACCTATGAAATGGATACTCAGAGAGTTATGTCAAA
GCGTAAATTAAGAGAGTTAGTGAAGACTGTGCGAATTGATGAGGGTGACG
GTGAAACTGTCAATTGACGGTGATGTTGAGGAATTACTATTGGATCTTGCC
GACGATTTTGTTACTAATGTTACAGCTTTTTCTTGATGATTGGCAAAACA
CAGAAAATCGGACAATTTGGAGGCAAGAGACATTCAAGTTACATTTGGAGA

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GAAATTGGAATATTAGGATTCTCTGGTTATTCCGCAGACGAAATAAGAAGT
ACAAGAAAATGGAATCCCTCTCAAAATTATAACCAGAAATTGCAGAGTAT
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GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

MSSNPENSGVNNANNNTGTGNADAITGAQQNMVLQPRQLQEMAAKFRTLLT
EARNVGETTPRGKELMFQAAKIKQVYDALTLNRRRQQAAYNNTSNSNS
SNPASIPTEVPNSSQQQQQQQQQTRNNSNKF SNMIKQVLTPEENQEYEK
LWQNFQVRHTSIKEKETYLKQNI DRLEQEINKQTDEGPKQQLQEKKIELL
NDWKVLKIEYTKLFNNYQNSKKTFFVECARHNPALHKFLQESTQQQRVQQ
QRVQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
ALKSQQQQQNTITATNNPRGNVNTSQTEQSKAKVTNVNATASMLNNISS
KSAIFKQTEPAIPISENI STKTPAPVAYRSNRPTITGGSAMNASALNTPA
TTKLPPYEMDTQRVMSKRKLREL VKTVGIDEGDGETVIDGDVEELLLDLA
DDFVTNVTA FSCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSAD EIRS
TRKWNPSQNYNQKLQSITSDKVAAAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTTTCGCTACAGGTGTTGT
TATTATTGTTGTTGTGCTGTTGTTTATTGTGCTATACTTGTGGTATTTAT
TCTGGACTTCCGATCGGAAATTTCTTCCCTTGAAGACCTTTTGAAGACA
ACAGTTATATATCATTGATCTGAATTTCTCAGGCTATTTTCAAAATTCCA
TACCTCCTTATTCCAACATTTGCTCGACTACTATAGAAAAGCCTTATTCT
TTTATCTTTGAAAGAAAGAAAAGGTGTCATAGCAAAAGTTTATTGTTACT
CTGTTTTGATATACTCCCTCTTATTCTGTGGAAGTATAAGATTGATTTGC
ATAAATTAACCAATCATTTTGCTACTTTCCCGGTTCTCCCTTTATTATAA
ACACTTTCAGAAAAATATTCTGCTACTATTCCTTACTTTACTATAAGAATT
TTGTTTTTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATA
ATGGCTAACGTAGAAAAACCAACGATTGTTTCAGGCTTTCCCGTTGTTGA
CTTGAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAAGAAATAG
AAATGGAAACGGATGATTACACCGATTTTATTAAATGTCATCATCAGCTTCC
AGAGAAAACCTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA
GATCATTACCACAAATAATAATATGAACTCCAAGATTAACAAGCAACTGG
ACAAGTTGCCCGAAAATTTAAGGCTTAATGGTAGAACCCCAAGTGGGAAA
CTAAGGTCATTTGTTTGCGAGGTTTGTACGAGAGCGTTTCGCAAGACAAGA
GCACTTGAAAAGACATTACAGATCGCATACAAATGAAAACCTTATCCCT
GTGGCCTCTGCAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT
GCTCAAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA
GAAAGTGTCGAGAACTATAACTAAAGCTCGGAAAAATTTCTGCATCCTCAG
TCAAGTTTCAAACCTCAACCTATGGTACTCCAGATAATGGTAATTTTTTG
AATCGCACTACTGCCAATACAAGAAGAAAAGCAAGCCCTGAAGCTAATGT
TAAACGTAAGTACTTGAAAAAACTGACGCGCAGGGCTTCATTTAGCGCAC
AATCAGCATCCAGCTATGCTTTGCCCGACCAATCTTCGCTAGAACAACAT
CCAAAGGATCGTGTTAAATTTTCTACGCCTGAATTAGTTCCACTTGACTT
GAAGAATCCTGAACTTGACTCTTCGTTTGACCTGAATATGAATCTAGATT
TAAACCTAAATCTAGATTCCAATTTCAATATAGCATTAAACCGTTCTGAT
TCTTCTGGATCAACAATGAATTTGGATTATAAATTGCCCGAATCAGCAAA
TAACTACACATATTCTCCGGCTCACCAACCCGCGCATATGTCGGCGCTA
ACACGAATTCTAAGAACGCTTCATTTAATGACGCAGACTTATTGTCGTCG
TCGTACTGGATAAAAAGCCTATAATGATCATTTGTTTTTCAGTATCTGAAAG
TGATGAAACTTCTCCAATGAACTCTGAATTAAACGACACTAAATTAATCG
TCCCAGATTTTAAATCGACTATACATCATTTGAAGGATTCAGGTCCCTCC
TCTTGGACTGTTGCTATAGATAATAATAGCAATAACAATAAGGTATCAGA
CAACCAACCTGATTTTCGTCGATTTTCAAGAACTGCTGGATAATGATACTT
TAGGTAATGATTTGTTAGAGACCACTGCCGTTTTTAAAGAATTTGAACTT

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TTACATGATGATAGCGTAAGTGCTACCGCCACGTCAAATGAGATTGACCT
TTCCCATTTGAACCTATCAAACCTCTCCAATTTCTCCTCATAAGTTAATTT
ATAAGAATAAAGAGGGGACCAATGACGATATGTTGATTTCTTTTCGGACTC
GATCATCCTTTCCAATCGCGAAGATGATCTGGATAAGCTATGTAATATGAC
CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAAGAGTCTA
AACGATCCCTGGAAGACTTTTTATCAACGTCAAACAGGAAAGAAAAGCCA
GATAGCGGCAACTATACTTTTTATGGGTAGATTGTTTAACGTTATCGAA
AATATCAAGAGCTCTGCCGGCTCCACTGTGAACAACAATCAGCCATCGC
ATTCCATAGAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT
AAAGTGCTTAGATACTATGAAAAGTTCAGTCATGATAGTAGTGAGAGTGT
CATGGACTCTAATCCAAACTTGCTGTCCAAAGAATTGTTAATGCCAGCTG
TGAGTGAATTGAACGAATATTTAGATCTTTTCAAGAATAATTTCTTCCC
CATTTCCCTATTATTCACCCAAGCTTGCTTGATTGGATTGGATAGCTT
GCAACGATATACTAATGAGGATGGGTATGATGACGCTGAAAACGCGCAGT
TGTTTGATCGATTAAAGTCAAGGGACAGATAAAGAATATGATTACGAGCAC
TATCAAATCTTGTCATTTTCGAAAATCGTTTGTTTACCCTTATTTATGGC
CACATTTGGTTCTTTGCATAAGTTCGGTTACAAATCTCAAACAATAGAAT
TGTATGAGATGAGTAGAAGAATTCTACATTCTTTTTTGGAGACTAAAAGA
AGGTGTCGCAGTACAACAGTAAATGACAGTTATCAGAACATTTGGTTGAT
GCAATCCCTAATATTGAGCTTCATGTTTCGCTCTAGTTGCTGATTATTTGG
AGAAAATTGACTCCTCTTTGATGAAAAGGCAATTGTCCGCATTATGTTCA
ACGATCAGATCAAACCTGTTTACCGACAATTTCTGCAAATCTGAGAAGAG
TATCAATAATAACAATGAACCTTTAACATTTGGTTCTCCTCTTCAATACA
TCATTTTTGAGTCAAAAATTAGATGCACCTTAATGGCTTATGATTTTTGT
CAGTTCTTGAAATGTTTCTTCCATATTAATTCGATTTGTCTATAAAGGA
AAAAGATGTTGAAACCATTTATATTCCCGACAATGAGTCAAAATGGGCCA
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GATTTTAGAACTTTTATTACAGTTTCACGTATGGACACTTACACTCAAT
ACCAGAATTTTTAGGGTCATCTATGATTTATTATGAATACGATTAAAGAA
AAGGAACCAAAATCACATGTGTTTTGGATCGAATCGATACGAAAAGGCTA
GAGAGGAGTCTTGACACTTCTTCCATGGCAATGATAATATGGCAGCAAC
CAATAAAAATATTGCGATCTTAATTGATGACACCATAATTTTGAAAAATA
ATTTAATGTCAATGAGATTCATCAAACAGATTGATCGCTCGTTTACTGAG
AAGGTTAGAAAAGGACAAATAGCAAAGATATATGATTCCTTTTTGAACTC
TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATTGTGTGAAT
TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTTCGTCTTTATACGTA
GAAGAAGAAAGTGATTGCTCCCAAAGAATGAATTCTCCAGAGCTGCCAAG
GATCCACCTGAATAATCAAGCGCTTTCTGTCTTCAATTTACAAGGCTATT
ACTATTGCTTCATCCTAATTATCAAATTTTTATTGGATTTTGAAGCAACT
CCAAATTTTAAGTTACTGAGAAATTTTTATTGAGTTGAGAAGCCTTGCGAA
TTCTATTTTACTTCCCACACTTTCAGATTGTATCCGCAAGAGTTTTCTG
GATTTCCCTGATGTTGTATTTACGCAACAATTTATAAATAAAGATAATGGT
ATGCTTGTCCTGGTTTATCCGCAAATGAACACCATAATGGTGCAAGTGC
AGCTGTTAAGACTAAGTTAGCCAAAAAGATCAATGTTGAAGGGCTTGCAA
TGTTTATTAATGAAATCCTAGTTAACTCTTTTAACGATACCTCTTTTTTG
AATATGGAGGATCCTATTCGAAATGAATTTTCCTTTGATAATGGGGACAG
GGCAGTGACAGACTTGCTCGTTCAGCACATTTCTATCGGATACCGGCC
TAGAAGGTATTAACCTCAGCGGCTTAAATGATTTCGCATCAAACGTCTCT
ACTTTGAATCTTTTACGTTACGGGGAAAATCATTTCATCAAAACATAAAAA
TGGTGGAAAGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAAT
ATGTTACTATTGCCAAGTTATTTTTTACCAATGTTAAAGAAAACATACATT
CATTTGTACATGTTAGATAAGATGGCAAGTGATTTCCACACTTTGGAAAA
TCATCTAAAGGGAAACAGTTGA

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YDR216W, 1323 aa (SEQ ID NO 110)

MANVEKPNDCSGFPVVDLNSCF SNGFNNEKQEIEMETDDSPILLMSSSSAS
RENSNTFSVIQRTPDGKIITNNNMNSKINKQLDKLPENLRNLNGRTPSGK
LRSFVCEVCTRAFARQEHKLRHYRSHTNEKPYPCGLCNRCFTRRDLLIRH
AQKIHSNGLGETISHTKKVSRITITKARKNSASSVKFQTPTYGTPDNGNFL
NRTTANTRRKASPEANVKRKYLLKLTRRASFSAQSASSYALPDQSSLEQH
PKDRVKFSTPELVPLDLKNPELDSSFDLNMNLDLNLNLDNLFNIALNRSD
SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNDADLLSS
SYWIKAYNDHLFSVSEDETSPMNSSELNDTKLIVPDFKSTIHHLKDSRSS
SWTVAIDNNSNNNKVSDNQPDFVDFQELLDNDTLGNDLLETAVLKEFEL
LHDDSVSATATSNEIDLSHLNLNSNPI SPHKLIYKNKEGTNDMDLISFGL
DHPSNREDDLKLCNMTRDVQAIFSQYLKGEESKRSLEDLSTSNRKEKP
DSGNYTFYGLDCLTLSKISRALPASTVNNNQPSHSIESKLFNEPMRNMCI
KVLRYYEKFSHDSSESVMDSNPNNLSKELLMPAVSELNEYLDLFKNNFLP
HFPIIHPSLLDLDSLQRYTNEDGYDDAENAQLFDRLSQGTDKEYDYEH
YQILSISKIVCLPLFMATFGSLHKFGYKSQTIELYEMSRRILHSFLETKR
RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEKIDSSLMKRQLSALCS
TIRSNCLPTISANSEKSINNNNEPLTFGSPLQYIIFESKIRCTLMAYDFC
QFLKCFHFHIFDLSEKEDVETIYIPDNESKASESIICNGHVQKQNFY
DFRNFYYSFTYGHLSIPEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL
ERSLDTSSYGNDNMAATNKNIAILIDDTIILKNNLMSMRFIKQIDRSFTE
KVRKGQIAKIYDSFLNSVRLNFKNYSVEVLCEFLVALNFSIRNISSLYV
EEESDCSQRMNSPELPRIHLNNQALS VFNLQGYCYCFILIIKFLLD FEAT
PNFKLLRIFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQQFINKDNG
MLVPGLSANEHNGASAAVKTKLAKKINVEGLAMFINEILVNSFNDSFSL
NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS
TLNLLRYGENHSSKHKNKGKGQGF AEKYQLSLKYVTIAKLFFT NVKENYI
HCHMLDKMASDFHTLENHLKGNS

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)

GGGTGCCGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC
TCTGCGCTACTCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG
TCTCCCGCGTACTGTACTCCATCTTTTTTTGGCGTTTTTCCCCTATCCAA
CTCGAACAAGGTTTGTTTAAATTTATTTTATTTTCTTTTCTTCGGTCGG
TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAGCGCATTTTTTTCTTTG
TCTTTTTGTTTTTTGTTTCTGTTCTCTGTTTTTTTACAAACCACGTCAG
GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA
CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTT
TGTTTTTCTTTTTTCACTGCTATAAGCCTTTAGACTAGTACTACAACTACA
ACAGCAACAACAACAACAAAACACGACTGGAAAAAAAAAATTAGGAAAA
ATGAATCCGGGCGGTGAACAAACAATAATGGAACAACCCGCTCAACAGCA
ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGGCAGCAGTTC
CTCAGCAGCCACTCGACCCATTAACACAATCAACTGCGGAAACTTGGCTC
TCCATTGCTTCTTTGGCAGAAACCCTTGGTGATGGCGACAGGGCCGCAAT
GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA
CATCTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA
GAATTATATGAAAGAGCACTTTTGGTAAATCCCGAACTATCAGATGTGTG
GGCTACTTTAGGTCATTGTTATCTGATGCTGGATGATCTGCAAAGAGCTT
ACAATGCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAACGTACCG
AAATTATGGCATGGAATCGGCATTCTTTATGACAGATATGGTTTCGCTCGA
CTATGCCGAAGAAGCTTTTGCCAAAGTTTGGAAATTGGACCCTCATTTTG
AAAAGGCAAACGAAATTTACTTCAGACTAGGTATTATTTATAAACATCAG
GGTAAATGGTCTCAAGCTTTGGAATGCTTCAGATACATTCTCCCTCAACC
TCCTGCTCCCTTGCAAGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTT
TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC
TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTTGTCT

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TTACGGTATGAGTAAACGTACAAATTTTATGACCCTCAAAGGCATTGGATT
ATCTTCTAAAGTCGTTAGAAGCAGATCCCTCCGATGCCACTACATGGTAC
CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATGA
TGCTTTTCCAACAAGCTGTTAATAGAGATTCAAGAAACCCTATCTTTTGGT
GCTCAATCGGTGTTTTATATTACCAAATTTCTCAATACAGAGACGCCTTA
GACGCGTACACAAGAGCCATAAGATTAAATCCTTATATTAGTGAAGTTTG
GTACGATCTAGGTACTCTTTACGAACTTGTAACAACCAATTATCTGACG
CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTTAC
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TATAAACAAATCGAACGGTGCGCCAACGAATGCCTCTCCTGCCCCACCTC
CTGTGATTTTACAACCTACCTTACAACCTAATGATCAAGGAAATCCTTTG
AACACTAGAATTTAGCCCAATCTGCCAATGCTACTGCTTCAATGGTACA
ACAACAGCATCCTGCTCAACAAACGCCTATTAACTCTTCTGCAACAATGT
ACAGTAATGGAGCTTCCCCTCAATTACAAGCTCAAGCTCAAGCTCAAGCT
CAAGCACAAGCTCAAGCACAAGCACAAGCTCAAGCACAAGCACAAGCACA
AGCGCAAGCACAAGCACAAGCACAGGCGCAAGCACAGGCACAAGCACAAG
CACAAGCACATGCACAAGCGCAAGCACAAGCACAAGCACAGGCACAAGCA
CAAGCACAGGCGCAGGCACAACAACAACAACAACAACAAGCAACAACAACA
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAAC
AGCAGCAGCAATTACAGCCCCTACCAAGACAACAGCTGCAGCAAAAGGGA
GTTTCTGTGCAATGTTAAATCCTCAACAAGGGCAACCATATATCACACA
GCCAACAGTCCATACAAGCTCACCAACTGCAACCATTTTCTACACAAGCTA
TGGAACATCCGCAAAGCTCTCAACTGCCACCTCAACAGCAACAACCTACAA
TCTGTTCAACATCCACAACAACCTTCAAGGCCAGCCTCAAGCCCCAAGCTCC
CAAACCTTTAATCCAGCATAACGTGGAACAGAACGTTTACCTCAAAAAGA
GATACATGGAAGGTGCAATCCACACTTTAGTAGATGCCGCCGTATCCAGT
AGCACCCACACAGAGAATAACACAAAGTCTCCTCGTCAACCAACCCATGC
CATTTCCAACGCAAGCTCCCGCAACAGGAATAACGAACGCTGAACCACAGG
TAAAGAAGCAAAAGTTGAACTCTCCAAATTCAAACATCAACAAATTAGTA
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ATCGCCAGCAGTAGTGGAGTCTAATACCAATAATACTTCACAAGAAGAAA
AACCTGTAAAAGCAAACCTCAATACCTTCAGTAATTGGCGCACAGGAACCT
CCACAGGAAGCTAGTCCTGCTGAAGAAGCTACCAAAGCAGCTTCTGTTTC
TCCTTCTACAAAACCGCTTAATACGGAACCAGAGTCATCTAGTGTCCAAC
CAACTGTATCATCAGAAAGTTCAACAACAAAAGCAAATGACCAAAGCACT
GCTGAGACCATAGAACTTTCTACTGCTACTGTTCTCTGCAGAAGCAAGCCC
TGTAGAAGACGAAGTAAGACAGCATTTCTAAAGAGGAAAACGGCACAACATG
AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT
GCTGAAAAACAACAAGATGAAACCGCTGCTACAACGATAAATCTGTAATCAA
ACCTACTTTTGGAAACAATGGAACACAGTGAAGAGGAGGCAAAATGCGTG
AGGAAGAGCAAAACATCTCAAGAAAAATCCCCACAGGAGAACACACTTCCA
AGAGAAAATGTAGTAAGGCAAGTGGAAGAAGATGAAAACCTACGACGACTA

A

YBR112C, 966 aa (SEO ID NO 52)

MNPGGEQTIMEQPAQQQQQQQQQQQQQQQQAAPVQPPLDPLTQSTAETWL
SIASLAETLGDGDRAAMAYDATLQFNPSSAKALTSLAHLYSRDMFQRAA
ELYERALLVNPELSDVWATLGHCYLMLDDLQRAYNAYQQALYHLSNPNPV
KLWHGIGILYDRYGSLDYAEAEFAKVLELDPHFEKANEIYFRLGIITYKHQ
GKWSQALECFRYILPQPAPLQEWDIWFLQGSVLESMEGWQGAKEAYEHV
LAQNQHHAQVLQQLGCLYGMSNVQFYDPQKALDYLLKSLEADPSDATTWY
HLGRVHMIRTDYTAAYDAFQQAVERNDSRNPIFWCSIGVLYYQISQYRDAL
DAYTRAIRLNPHYISEVWYDLGLTYETCNNQLSDALDAYKQAARLDVNNVH
IRERLEAQTQLKENPKNINKNSAGPTNASAPPVLIQPTLPNDQGNPL
NTRIISAQSANATAISMVQQHQHPAQQTPIINSSATMYSNGASPOLQAQAQAQA
QAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA

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QAAQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQLPLPRQQQLQKKG
VSVQMLNPQQGQPYITQPTVIAHQQLPFFSTQAMEHPQSSQLPPQQQQQLQ
SVQHPQQLQGQPQAQAPQPLIQHNVEQNVLPQKRYMEGAHTLVDAAVSS
STHTENNTKSPRQPTHAIPTQAPATGITNAEPQVKKQKLNSPNSNINKLV
NTATSIEENAKSEVSNQSPAVVESNTMNTSQEEKPVKANSIPSVIGAQEP
PQEASPAEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQST
AETIELSTATVPAEASPVEDEVQRHSKEENGTTASAPSTEEAEPAA SRD
AEKQQDETAATTITVIKPTLETMETVKEEAKMREEEQTSQEKSPQENTLP
RENVVROVEEDENYDD

YMR043W, 1361 bp, CDS: 501-1361 (SEQ ID NO 305)
AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCAAAAAGCTAGGGC
GTACTGTACTGGAATCTCTGCTTTTTTCTTTACCTTACTTCAATTTGCCCT
TGTCTGCTTTTTTACGTGTGTTTTGGCGTTTCTGCTTTTTCTTTTTTATTA
CTCGTTGTTGTAAATCATTTTCTAAGTATTATACATACTATATCATCGCA
TACCCAATCGGTTTCCTATTCTCACCACCTTTTTTCTGGAAAAATACATAG
CCTAACAAGCAATTTTATTTTACGTTTGTTAATTCATTATACTGATAATA
TTTTTGAATTTTTTTTTTTTTTTTGATACATTTTTTTTTTAATCGCTGTTTTGT
CTGTTTTTTTTTCGATTACGTTATAGGGAAAAAAACGGGAAAGGAAAGAGAA
AAAAAAATTAGTGCAGAGCAATAAGAAGCGAAAATCAAAAAAAGTTTTG
GATCTGCAAGACTTGCTGTACGCAACAATATTATAGCCACCCAGCAAAA
ATGTCAGACATCGAAGAAGGTACGCCTACTAATAATGGGCAACAGAAGGA
GAGAAGAAAGATAGAAATTAAGTTCATCGAGAATAAAACAAGGCGCCATG
TGACATTTTCCAAAAGGAAGCACGGTATCATGAAAAAGGCGTTTGAGCTT
TCTGTTCTAACGGGGACCCAGGTCTGTGCTAGTCGTTTCAGAAACAGG
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GAAGAAGACGAGGAGGAAGACGGTGATGATGATGATGATGATGACGATGA
TGGTAATGATATGCAACGCCAGCAACCACAACAACAGCAACCGCAACAAC
AGCAACAAGTATTGAATGCACACGCAAATAGCTTAGGCCATCTAAATCAA
GATCAGGTACCGGCAGGCGCGCTGAAACAAGAGGTGAAGTCACAATTGCT
AGGCGGTGCCAATCCTAATCAAACTCAATGATTCAACAGCAGCAACATC
ACACGCAGAATTACAAACCACAACAGCAACAGCAACAACAACCACAGCAG
CAAATGTCACAGCAACAAATGTCACAGCATCCTCGACCACAGCAAGGAAT
ACCACATCCGCAACAATCGCAGCCACAGCAACAGCAACAACAACAAC
AATGCAACAGCAGCAACAGCAGCAACAACAACAACCCCTCACCGGCATT
CATCAGCCTCACCAACAGGCTTTTGCCAACGCTGCCTCCCCCTATCTGAA
TGCTGAACAGAATGCTGCCTACCAACAATACTTCAAGAACCGCAACAAG
GCCAATACTAA

YMR043W, 286 aa (SEQ ID NO 306)
MSDIEEGTPTNNGQKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFEL
SVLTGTQVLLLLVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDDE
EEDEEEDGDDDDDDDDGNDMQRQQPQQQQPQQQQQVLNAHANSLGHLNQ
DQVPAGALKQEVKSQLLGGANPNQNSMIQQQQHHTQNSQPQQQQQQQPQQ
QMSQQQMSQHPRPQQGIPHPQQSQPQQQQQQQQQLQQQQQQQQQPLTGI
HOPHQOAFANAASPYLNAEONAAAYQOYFOEPOGOY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)
TTCCACGTTTCGCAAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG
TATATTAAATGCAGAAATCGTCTTATCATTATTGGGCTCTCTTAACGGCG
CAGCATCACCGGGTGATGAATGCCAAGCCGCAGAAAGAAAGAAAAAATTT
TACTTCAGATTTCTGATAAAAAATAAAACGGAAGAGATGAAAGCTAATAAT
AGAAACAGCTCGATCTTCTCTGAACAATAATAATTAAAGGACAGACAAA
AAGAAACGTAAGAAAGAAGCGAGCCTGTTCTAAAGTGTTCAACGACTGAT
TCAATTAGAAGTGCCTACTCTGATAGCCAACTCAACTTTTTGACTCGTTA

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AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTTTTTTCAAGGTT
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ATGGGTAGACGGAAGATTGAAATCCAGAGAATTTCTGATGACAGAAATAG
GGCTGTCACGTTTATAAAAACGTAAAGCTGGCCTTTTTTAAGAAGGCCCATG
AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGGTCC
AATAACACGTTCTATGAGTTTTCTCTGTGGATACGAATGATTTAATCTA
TCACTACCAAAATGACAAAACCTTGCTTCACGAAGTGAAAGATCCTTCCG
ATTATGGAGACTTTCACAAAAGTGCATCCGTTAACATAAATCAAGACCTA
CTCAGGTCGTCTATGTCAAATAAGCCTTCGAAATCAAATGTTAAAGGAAT
GAACCAGTCAGAAAATGATGATGATGAGAACAATGATGAGGACGACGATG
ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTCGAATAAAAAAGCC
TCTGATAAAAAATATACCGAGTGCACACATGAAGTTGTTATCCCCGACCGC
ACTCATTTCAAAGATGGATGGTAGTGAGCAAAATAAACGTCATCCTGAGA
ACGCGCTGCCGCCCTTTACAACATTTGAAAAGATTGAAACCGGATCCTTTG
CAAATAAGTAGAACTCCGCAACAGCAACAGCAGCAAAATATATCGAGACC
ATACCATAGTAGCATGTACAATCTTAACCAGCCTTCATCCAGTTCATCTT
CTCCTTCCACGATGGATTTTCCAAAATTACCAAGCTTTCAAACCTCTTCC
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ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCACCA
TCTAATCTTTGGAAGACTCTATTTCAGCAGACTGTCAAAGCAAGAAGGAA
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GCAGTAATTCGCTATTCCAAGTGAACCCCTCTCTGCCTCCTCCACATCG
GCCAACGGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAACAAAAC
AAGTAGGTCTAGCAAAATTTCTCCACTATCCGCATCTGCCTCAGGCCCCCT
TAACTCTCCAAAAGGTAATAATGGCAGAATGGTAATAAAATTGCCAAAT
GCAATGCGCCTAACGGTTCTAACAATGGTAATGGCAGTAACAATAACAA
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ACAAATGTCTTTCAA AAAACAGAGCCAAACAGTACCATTAACTACAACAT
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CCAACAGTGCCAAGCCGGGAAACACAAACAATCCTGGTACTTTCCCTCCC
GTACAGACGGCCGTAAACAACGGCAACTCCAGCAATATCAGCAGCACTAA
CAACACTAACAACAACAACAATAACAACAACAACAGCAGCAACAACA
ACAGCAACAACGGCAACGACAATAACAGTAACAATAGCAATAACAGTTAC
TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTTCAGAACA
TACTACCGATGGTGACTCGAACAATCAGTCCAACCTCAAGTACATATGATG
CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAT
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TTCAGGAGAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MGRRKIEIQRISDDNRNAVTFIKRKAGLFKKAHELSVLCQVDIAVIIIGS
NNTFYEFSSVDNDLIYHYQNDKNLLHEVKDPSDYGDFHKSASVNIQDL
LRSSMSNKPSPKSNVKG MNQSENDDDENNDEDDDDHGNFERN SNMHSNKA
SDKNIPSAHMKLLSPTALISKMDGSEQNKRHPENALPPLQHLKRLKPDPL
QISRTPQQQQQNI SRPYHSSMYNLNQPSSSSSSPSTMDFPKLP SFQNSS
FNGRPPPIISIPNKFSPFTNASSRTPKQEHKINNSGSNNNDNSNYTQSP
SNSLEDSIQQTVKARRKLSARPVLRVRI PNNNFSSNSAIPSEPSSASSTS
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVIKLPN
ANAPNGSNNNGSNNNHPYPFGSGSSPLFSATQPYIATPLQPSNIPGGP
FQQNTSFLAQRQTQQYQQMSFKQSQT VPLTTTLTGRPPSTFSGPETSNG

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PPTGSLPSKFVHDLMSNSPNVSSI SMFPDWSMGPNSAKPGNTNNPGTFPP
VQTAVNNGNSSNISSTNNTNNNNNNNNNNSSNNNSNNGNDNNSNNSNSY
YSNNEDAPVNGAAI SEHTTDGDSNNQSNSSYDAAATAYNGNTGLTPYIN
TAQTPLGTFKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)

AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTACCACTGTTACTGT
GCGCGTTTCGAGCGTAGCTTTTCGTGGTGAATTTATTGTAAGATTCTCCAGC
TGGCTCGATAGTTCTGCCTCCTGCGTATCCATATCCATTTCCGTATGCTT
TTACTATTCAACCTAGTCGGCAATTTTTCACCTGAATATTGTTGAACAC
TTCTGGCATCCTAGATACTCATCTGTATTTATTTCATTATCTGTTGTGCAT
CGTTAATAGCATTCCAGTAAACAAGTTTAGGTCACCTACCCGCATAAGCCT
TTTGCGCTTTGGCGTAACCCCTCCTCGCGAAAAGAAACGGGACGCAAAAA
AAAAACAACAAAACAAGAACAACAAAACAAAACAAATAGGACAGAGCCTTAA
GGAGCTGCAAGGATCTTCTGAATATTTGGCATCGGCATTGTGGGTGGAAA
AAGTGTCCAAATTGGAATAAATTGGTCAGAATAGAGCATTGATTCCAAC
ATGGACAGAGATATAAGCTACCAGCAAAATTATACCTCAACTGGGGCAAC
TGCAACTTCCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT
TTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT
ACAACGACTCAATTCACCCACGCCCTATTCTTCTAATCAGTATCAACAGAC
TCAAGATCATTTTGGCAATACAGACGCTCACAACAGTTTCGAGCAACGAAT
CGTCGTTGGTAGAGAACAGTATATTACCGCATCATCAGCAGATACAACAG
CAACAACAACAACAACAACAACAACAACAACAGCAAGCTCTAGGTTCT
ACTTGTACCTCCTGCTGTCAAGGACAGATACAAGTGAGACTTTGGACG
ATATCAACGTTCAACCTTCTTCTGTTTTCAGTTTCGGCAACTCTTTACCC
AGCGAATTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTGTGGA
CTCTCCGTCACCAATTTCAATTTCTTTCACAAAACCTCCGGCAAAGACAC
CACTTCGATTTGTAACAGATTCTAACGGTGCTCAGCAAAGCACCACAGAG
AACCCAGGTCAACAACAGAATGTTTTAGCAATGTCGATTTGAACAATCT
TTTGAAGAGTAATGGAAAAACACCCCTCATCTTCATGCACCGGCGCATTTT
CACGCACTCCTCTGAGTAAGATTGACATGAATCTCATGTTCAATCAACCG
CTGCCGACATCTCCATCAAAAAGGTTCTCCTCCCTGTCGTTGACACCATA
TGGAAGCAAAAATCTGAATGACGTCGGTACACCTTATGCAAAAGCATTGA
TATCGTCTAACAGCGCGTTAGTGGATTTTCAGAAGGCAAGAAAGGATATT
ACCACTAATGCAACATCCATAGGGCTGGAAAATGCCAACAACATCTTACA
GAGAACGCCGCTAAGATCTAACAATAAAAAATTATTTATTA AAAACCCCC
AGGATACCATCAATAGCACTAGCACACTAACTAAGGACAACGAAAATAAA
CAGGACATATACGGCTCTTCACCGACTACCATCCAATTAAATTCATCAAT
AACTAAATCTATCTCCAAATTGGATAACTCTAGAATTCCTTGTAGCTT
CGAGATCAGATAACATTCTGGATTCCAATGTGGATGACCAATTGTTTGAT
TTGGGGTTGACAAGATTACCTTTATCACCAACACCAAATTGTAATTCTTT
GCATAGTACAACCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA
AGATGGGGTCTTTTAGAAGTGATACGGGAATCAATCCAATTTCAAGTTCA
AACACAGTTTCTTTTAAGAGCAAATCAGGCAATAATAATTCAAAGGGTCG
AATCAAAAAAATGGGAAGAAACCTTCCAAATTTCAAATTATTGTGGCAA
ATATTGATCAATTTAACCAGGATACATCATCGTCATCTTTATCATCATCA
TTGAATGCAAGTTTCGAGTGCAGGGAATTCAAATTCAAACGTAACAAAGAA
AAGAGCAAGTAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT
CGAAATCACAAGCAAGGAAAAGCTGTAATTCTAAATCTAATGGAAATTTA
TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)

MDRDISYQQNYTSTGATATSSRQPSTDNNADTNFLKVMSEFKYNFNSPLP
TTTQFPTPYSSNQYQQTDHFANTDAHNSSSNESLVLNSILPHHQQIQQ
QQQQQQQQQQQALGSLVPPAVTRTDTSETLDDINVQPSSVLQFGNSLP
SEFLVASPEQFKEFLLDSPSTNFNFHKTPAKTPLRFVTD SNGAQQSTTE

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NPGQQQNVFSNVDLNNLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQF
LPTSPSKRFSSLSLTPYGRKILNDVGTPYAKALISSNSALVDFQKARKDI
TTNATSIGLENANNILQRTPLRSNNKKLFIKTPQDTINSTSTLT KD NENK
QDIYGSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILD SNVDDQLFD
LGLTRLPLSPTPNCNSLHSTTTGT SALQIPEL PKMGSFRSDTGINPISSS
NTVSFKSKSGNNNSKGRIKNGKKPSKFQIIIVANIDQFNQDTSSSSLSSS
LNASSSAGNSNSNVTKKRASKLRSQLLSDSGSKSQARKSCNSKSNGNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)

TTTCTTCAACAACGACGAGTTAACTATTGTGCTCTTTTTTTGAGCCACCA
AATACACTCCATTCCAATAGCTTCGCACAGTGAGGCGAAAATTTTGGAAC
AGCGCTAATGAATTATTTGTGAGCTCGGCGAGTTCAAATTTGAAGAAAAC
GCGGTTGGGTCGTAACTATGGTTAGACGCTCAATGTCGCCC GAAAGGGA
AGGCTGTTCTCACTTTTTTCGCGCGTTGCACCCTTTCTTCCGCGAAAAAT
GAGAACGATGGATTTAAAATCAAGAGAATTGGCCTTAGTAGTGGCAAATA
CTACCTTGGTTGGTTATCTTGTAACGATTGGTAAGAAAGGGGCATCTCTG
TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGGTCAGA
TTTATTAAAGACGTTTCTCTTTCCGCATTTTCGATTATTGTTATATTAA
TTTATCCTATATAGACAAGTCAAACCACAAATAAAACCATACACACATACA
ATGTCTGCTAAAGCCGAAAAGAAACCAGCCTCCAAAGCCCCAGCTGAAAA
GAAACCAGCCGCTAAAAAGACTTCCACTTCCACTGATGGTAAGAAGAGAA
GCAAGGCTAGAAAGGAAACATACTCTTCTTACATTTACAAAGTTTGAAG
CAAAC TCACCTGACACTGGTATTTCCCAAAAGTCCATGTCTATCTTGAA
CTCTTTCGTTAACGATATCTTTGAAAGAATCGCTACTGAAGCTTCTAAAT
TGGCTGCGTATAACAAGAAGTCTACTATCTCTGCTAGAGAAATTCAAACC
GCTGTTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGTCTCTGA
AGGTA CTAGAGCTGTTACCAAGTACTCTTCCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)

MSAKAEKKPASKAPAEKKPAAKKTSTSTDGKKRSKARKETYSSYIYKVLK
QTHPDTGISQKSM SILNSFVNDIFER IATEASKLAAYNKKSTISAREIQT
AVRLILPGELAKHAVSEGTRAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)

ACCAACCAACTTCTTCTTTGTCTCTCAATATCAAAGAAAAAAAAAAAAAAC
CCACTGCTCAGATGTTATAAGGAAGGGGTGTTAACTTATATACAGGTTCA
TCTACCAGTCACCAGTCCATACAAACTTGAACCGTCTGCGTACCAGTCCT
AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTCAATGCTTCAG
TTCTGCCATTGAGACTGTGCAATAGAAATTTCACTACCACAAGAATATCC
TACAACGT CATACAAGATTTGTATTTGAGGGA ACTAAAAGACACCAAAC
GGCTCCAAGTACCTTGCAAGATGCTGAAGGTAATGTTAAGCCTTGGAACC
CACCACAAAACCAAATCTACCAGAATTGGAAC TTCAAGGCCAGAGGCT
TTAAAGGCTTACACCGAGCAAAATGTAGAACTGCTCATGTTGCTAAAGA
GTCTGAAGAGGGTGAGTCAGAGCCAATTGAAGAGGATTGGCTAGTTTTGG
ATGATGCTGAGGAAACCAAAGAAAGTCATTGAAC TTTTCATAGCATCCTC
CTTGTCGAAGAAAAACAAACAGAACCACAAGCTGAACAAGATCATTATT
TTTGGCTTTCTTCTCTCATCTTTTATATTCGAATCCAGTACAATAAAG
AAAAAGCAAATACTACTACGCACTCTTTGTAATCAGCCACACAAAATGCA
GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGCTTTTAT
CTTTCCTATTACTACTATTCTTTTATTTCAATAACTATTACTTTCTAAGT
ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 109aa (SEQ ID NO 282)

MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIFESSTIK
KKQNTLRLCNPQPKMQNLFFKQKIQLYIDTSLSFLLLLFFYFNYYFLS

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MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTCAGTTATTTACCTTCCTTCTCTCACGTGTAAATATTTGTGTGTC
ATACACACCGCTAAAAACCTTTGCATCAACTTATACCCTACATTTCTATA
GACGCTATTTGGAAACAAGATGTAACCTTTTTTTCTTTTAGTTTGTGAGA
TTTGTACTCGTAAAGAGTACGTTTATTTATTTATTCAAATTTTATCTTC
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA
GAATTGCTGACGCTTACAATTGCTTTATTGTTTGATTATATGCACGTATA
CATATAGTGTGAGCAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC
GCGCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGCGG
ATAGAAATAAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA
ATGGCTAATAAAGTTATTCAACTACAGAAAATCTTCCAATCTTCCACTAA
ACCTCTATGGTGGAGACATCCAAGGTCAGCTTTATACCTGTATCCATTTT
ATGCTATTTTTGCGGTAGCCGTCGTTACACCACTTCTATACATTCCAAAT
GCTATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSSTKPLWRRHPRSAlylyPFYAIFAVAVVTPLLYIPN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATACGTATGTTTTTTTAGATTATGCACCTTCTTTGCCACAGTAAA
TGTGGCGGGGAAGATGTTGAGCTAGCGCCGTGCACAGTGGAAAGAGACGGA
GGCGATTGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCCTACACCGTG
TTGAGCCACCCCCCCTCAGGAGTAAATTTACACAAACAGTGGTGGTGCC
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT
TTTGTAGGCGTTTATGGATATGGTATGGATATGGTATGGCTTGAGGTAGG
TAATCCAGACACCACTGGAAATATATATAAGGAGAGAGTTCTGGCAGGTA
GATTTGTACTCCTCTCTACCACTTTCTTCTACTCCTTTTATTATGTAATG
TTTATTATAAGCACAGCAAAAACGTTAAATAAATCTAATAAGATTTTCATT
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAATTCAAAC
ATGACCAGAAGCTAGCAAATGGACAGTCCACGAAGCAAAGTCTAACCCTAAA
GTATTTACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAAGA
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGCCTGGCGATGAGATTAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTGATTTGCAACAAT
ACCACATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKWTVHEAKSNPKYFTHNGNFGESPNHVKRGGYKGNWGPDEIN
DLIDSGEIKTVFNKTRRGSNSQNNERRLSLQQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTCATGCGCGCAATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA
AACAAATGCAGCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT
GTAGAAAAAGATGACGCCCTGGCAGAGAGGTGGGGGAATTGAGGGGTCTT
CGCTACCCACCTTAAGTATGGAAGAATATGATGAAGAATATGATGATAAC
TCTTGGAAGCGAGCGGGCGGGTCCATCACTTTTTACGGATTGGTAACACA
GGGGCCTCAGTTCGATACTTGGTATTCAGGCTTCCAGCGTTGGTGAGTTT
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC
GTTAGGTGAATTGAGCAGTAGCGATATTAGATATATTTAGTATTTTATAG
CGTCTTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG
GGACTGTTCGATATCGCAGATACTAGAGTATAAATTTGATTGAGGCGAG
ATGACAACATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

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CCCCCCAAACAGAAGTATCTGGATCCGATACTGTTGGGGACCAGCAATG
AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTCCCGAATTAATGAC
ACGGCGTGGACTATTGTGTATAAATCGCTGTTGGTGGTTCATTTGATGAT
AAGGGAGGGTTCCAAAGATGTTGCATTGCGGTACTACTCTAGGAACCTGG
AGTTTTTTGACATTGAAAACATACGTGGCTCCAATGGCAGTGCGTCTGGA
GACATGAGGGCACCTTGATAGATACGATAATTATCTGAAGGTGAGATGCAG
GGAGTTTGGTAAATCAAAAAGGACTATGTGAGAGACGGCTATCGAACAC
TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT
ATCAATATAGCACTAGATCATGTGGAGTCCCTAGAGGTACAAATACAAGC
CCTGATTA AAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA
TATTTGGTTTCAAGCTGCTTATTCAAGACCTGCTAGCGCTATATAATGCT
CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACCTATCTCA
TCATAATGCAGAGAGAACTCTAGACCTGTACAAGACGTTTGTGATTTGA
CCGAGCACGTTGTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTGA
ATACCCGTCATCAAGCATATCACTACCAAACCTGGTCAGATCGCTAGAAGA
ACATCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA
GTTCTCAAGGAAGTGCTGGGGCCGTAGTAGCCAAATCTACTGCACAGGAA
AGGTTGGAGCAAATCCGGGAACAAAAAAGGATACTAGAGGCACAATTGAA
AAACGAACAAGTAGCGATTTCCCTGCTCTAACTACTGTACGCGCGGCTC
AATCTTACAACCCGTTTGGAACAGACTCTTCTATGCATACTAACATTCCA
ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC
TCAAACTCAGCCACAGGTGATGAATACACCAACCGCTCATACAGAGCCCG
CAAATTTAAACGTTCTCTGAATATGCAGCGGTCCAACACACAGTGAACCTC
AACCCTGTACAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTC
GATTAACAACCATTTAACACCCACATTTACAGGTGCAGGGTTTGGAGGAT
ACTCCGTTTTCACAGGATACAACCTGCCGCTTCTAATCAACAAGTCTCTCAT
TCACAAACTGGTTCTAACAACCCGTTTCGATTGCACAACGCCGCGACGAT
CGCAACAGGGAATCCTGCACACGAAAATGTCTTAAATAACCCATTTTCAC
GACCAAACTTTGATGAACAAAATACCAATATGCCGCTACAACAACAGATA
ATAAGTAACCCTTTTTCAAACCAAACGTACAATCAACAACAATTTCAACA
ACAAAAAATGCCTTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA
GCATGCAGGGATCGATGAATATTCTCAGCGTTTGTATAAATGGAATTT
CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA
GCAACAACAGCAACAGCAACAACAGCAACCACAACAGGGTTATTATGTGC
CTGCAACTGCAGGAGCCAACCTGTTACAAATATAACTGGGACAGTTCAA
CCTCAAAATTTCCCTTTCTATCCACAACAGCAACCACAACCGGAACAGTC
TCAAACACAGCAACCAGTTTTAGGAAACCAATATGCTAACAACCTCAATT
TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPIILLGTSNEEDFYEIVKGLDSRIND
TAWTIVYKSLLVVHLMIREGSKDVALRYYSRNLEFFDIENIRGSNGSASG
DMRALDRYDNYLKVRCREFGKIKKDYVRDGYRTLKLNSGNYGSSRNKQHS
INIALDHVESLEVQIQALIKNKYTQYDLSNELIIFGFKLLIQDLLALYNA
LNEGIITLLESFFELSHHNAERTLDLYKTFVDLTHEVVRYLKSGKTAGLK
IPVIKHITTKLVRSLEEHLIEDDKTHNTFVPVDSSQGSAGAVVAKSTAQE
RLEQIREQKRILEAQLKNEQVAISPALTTVTAAQSYNPFGTDSMHTNIP
MAVANQTQQIANNPFVVSQTQPPVMNTPTAHTEPANLNVPEYAAVQHTVNF
NPVQDAGVSAQQTGYYSINNHLTPFTGAGFGGYSVSQDTTAASNQOVSH
SQTGSNNPFALHNAATIATGNPAHENVLNPNFSRPNFDEQNTNMPLQQQI
ISNPFQNTYNQQQFQQQKMLPSSINSVMTTPTSMQGSMNIPQRFDKMEF
QAHYTONHLQQQQQQQQQQQQQQQQQQPQQGYYPATAGANPVTNITGTVO
PQNFFPYFPQQQPQEQSQTQQPVLGNQYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCTGACTTTCCCATCATACGACGATGCTCTAGTAACTTGCACC

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CGCACCTGTTAGATAAACAAGTGCGCCCAAGATCACAATACCGAAGGGGC
GATATCACCACCTCAGTATTCTACAGTCGAGCATAGCGTAGTCTGGCAGTA
TCCCGCACGATCCATTGTATTGTTGTCCAAACCGCATTTTATGTGTAAC
GATTAATCGTATATACATGGCCTACAAGAAATTACCCTGCGGCGAAGGGT
GAAAAAAAAGTAGTGGAAGCTAAAGAAAGAAGAGTTTAGTTACGGACCC
TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATTGACCTTTGT
TGAAGGAGGCGTTTCGTTTATTTAATTATTTTGTTCTGTTTTGCCTACAAC
TGCGAATACGCTCACATTCTAGTTTGACCTTCACAAATTCCTTATCATCTT
CTTTTGTATTATTTTGACACACCCCTATTAAGTGTATTTGTTTTGTAAGTA
ATGTCTAAGCAGTTTGTTCGTTCTGCAAAGAACATGATGAAGGGCTACTC
ATCCACACAAGTGCTTGTGAGAGATGCCACGGCGAACGACTCGAGGACTC
CATCGATAGACACTCTCGACGATTTGGCACAGAGATCTTACGATTCGGTG
GACTTCTTCGAGATTATGGATATGTTAGACAAGAGGCTGAACGATAAGGG
CAAATACTGGAGACACGTTGCCAAATCGCTGACCGTTTTGGACTATCTTG
TTCGTTTCGGGAGTGAGAACTGTGTGCTATGGTGCAGAGAGAATTTTAC
GTAATTAAGACATTAAGGGAATTCAGACACGAAAATGAGTCCGGATTTGA
CGAGGGACAAATTATCAGAGTAAAGGCTAAAGAACTCGTCTCTTTGTTGA
ATGATGAAGAAAGGCTACGCGAAGAGAGGTCTATGAATACAAGAAACAGA
AGGGCGAACAGAGCTGCTAGGCCAAGGCCAAGAAGACAAAGAACAAGGAG
CAACCCACACGATTCTTCTCCCTCTTACCAGGACGATTTGGAAAAGGCCC
TAGAGGAGAGCAGAATTACTGCTCAAGAAGATGAACAACGTAGAAGAGAA
CTGGCCCAGTACGACGATGAAGATCCTGACTTCCAAGCTGCCTTACAACT
AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACCTACAGAGATTAC
AGAAGCAACAACAGTCTCTGTCTCAATTTCAAGCTCCTTTACAACAACAA
CAACCACAACAACACAGCGTACTACGACATTTTCGGTAATCCAATCTC
CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA
TGGCTCAGCAAAGATGGCTGGACCAGCAGCAAGAACAACAGCAGCTTGCT
GAACAACAATATTTTCAGCAGCAACAACAAGCTGCGGCCGCGCTTCTGC
CTTGCAACAGCAACAACAAGCCGCTAATATGCAACAACAACAACAACAGC
CCGCTGATTTTTCACAACCTTTGCCTACAGGTTCTAATAATCCGTTTTTCC
ATGGATAATCTTGAAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA
AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC
AATTGCAAAGACAACAACAAGAGGAAGCTCAATTACACCAGAAGAGGCAA
GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC
CCAGTTCAGCAACAACAACCCCTTGAAGCAAACAAGGACTGGGAACCAGT
CTATATCGGATAAATACAGCGACTTGAATACCTTGTTAGCAACTGGTACA
GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCCTGCACAACA
TACAAAGACAGGCACATTTATAAATTCTCAGGGTACAGGCTACAAACAGG
TTACTAATGAACCAAGAACAACCCCTTCTTAAGCAACCAATACACTGGT
TTACCAAGCACAAATATCGTGCCACGCAAACAGGGTACGGGTTTGGTAA
CCAACCTCAAAGTCCTCCTACTAATTCTCCTCAGCAAAATCCTACTGGTA
TAAGTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCGCAA
TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCCAAACTTCCA
ACAACAACCACAATACACTCAAAATTATCAACAACAACCACAATACATTC
AACCTCATCAACAACAACAGCAGCAGCAGCAGCAACAGCAGCAACAG
GGATATACTCCTGACCAAGGTGTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRS AKNMKGYSSTQVLVRDATANDSRTPSIDTLDDLAQRSYDSV
DFFEIMDMLDKRLNDKGKYWRHVAKSLTVLDYLVRFGSENCVLWCRENFY
VIKTLREFRHNESGFDEGQIIRVKAKELVSLNDEERLREERSMNTRNR
RANRAARPRRRQRTRS NPHDSSPSYQDDLEKALEESRITAQEDQRRRE
LAQYDDEDPDFQAALQLSKEEEEELKQLQELQRLQKQQQSLSQFQAPLQQQ
QPQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMAQQRWLDQQQEQQQLA
EQQYFQQQQQAAAAASALQQQQTAANMQQQQQPADFQQPLPTGSNNPFS
MDNLERQKQEQQHAQLQRQQEEARQQQEQLKLQQLQRQQQEEAQLHQKRQ

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EEAQLQQQQAQLLQQQAQFQQQQPLKQTRTGNQSIDKYSIDLNTLLATGT
GIDTFGNTGEARIPAQHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG
LPSTNIVPTQTGYGFGNQPPSPPTNSPQQNPTGISYSQPQQQQQFQQQPQ
YMQNFQQQPQYAQNFPQQPQYTONYQQQPQYIQPHQQQQQQQQQQQQQQ
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)

CACTTCTCAGAAATGCATGCAGTGGCAGCACGCTAATTCGAAAAAATCTC
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTTATGAC
CCACTACTTCTCGTAGGAACAATTCGGGGCCCTGCGTGTTCTTCTGAGG
TTCATCTTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA
AAAATTAGATGGCAAAAAGTCGTCTTTCAAGGAAAAATCCCCACCATCTT
TCGAGATCCCCTGTAACTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA
ATACAAAATATACTAGAACTGAAAAAAGTATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTTCAATCTATTCTTCATTTGCAGCTATTG
TAAAATAATAAAACATCAAGAACAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAAAAGTTTTTTTAAATTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACCTCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACCATCAAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTTCGTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTTCATCAGAAGATTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAACTGGTTT
GATTGTCTCCATTTTCAACATTTGGTTGTGCCATTGGTGGTATTATCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCTGTTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATTATTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCTCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTTACTGTACCAACTTCGGTACTAAGAATACTCCAACCTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTCGTCGTACTTGTGTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAAGTGTATGATTGTCTTGCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAAACTTTCCCATGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACCTTCTACTACGGTTACGTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTTCCACCATCCAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGACTCACGATGACAAGCCATTGTACAAGAGAATGTT
CAGCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)

MSQDAALAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPAAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTFIRRFG

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MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVLIVVV
VIYIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLA EVEAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANLWLGFLIGFFTPFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMTHDDKPLYKRMFSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAAAAATGTTTTTTAGGCAACGGAGATTTCGTTTATCCACGTTTACCCC
ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAACAGTTTTT
TTCCTTTAAACGCTGGAAGGAGAAATTATTGGAACCTTTCAGAGA
ATAGTCCGTAGGCAAATTGAAAATGTTCCTTAAAAAATTTTCGTTTCTTAC
TCATTGAGATTATTCAGATGCCCTCCGTGCCTTCATTGAAAAAATCCAA
GAGATGCTCGGATCTGTATGCAGATTTTGGCTTGCAGACAATGGAGAGC
AAATGGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG
AAAAGACATATGGTTTGTAACTATCTTCTTCTTTTTTCCAATTTTTCTGT
TTTAATAATAAAAAACAAGAACAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAAAAGTTTTTTTAATTTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACCTCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAACAAG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTTCAAAGAGACCAGCTTCTGCCTATGTCACTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTCATCAGAAGATTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCTGTTGT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCCTGGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGT
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTTCGTCGTACTTGTGTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAAGTGTATGATTGTCTTTGCCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACCTTCTACTACGGTTACGTTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTTCACCATCTAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGGCTCAGGATGATAAGCCATTGTACAAGAGAATGTT

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CAGCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAALAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTD FIRRFG
MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGLIVVV
VIYIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVS NKVAVDDPSVLA EVEAVLAGV
EAEKLAGNASWGELFSSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKA VGLSDSFETSIVLGI VNFASFVFGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSK GAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTPFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTCGGCATCCACTAAATATAATGGAGCCCGCTTTTAAAGC
TGGCATCCAGAAAAAAGAATCCCAGCACCAAATATTGTTTCTTCA
CCAACCATCAGTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG
GGGCACAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACC
TGCCTGGAGTAAATGATGACACAAGGCAATTGACCCACGCATGTATCTAT
CTCATTTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGAAAA
AGCTGAAAAAAGGTTGAAACCAGTTCCTGAAATTATTCCCTACTTG
ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAATTCTGTAAATCT
ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTAGT
TTTAAAACACCAAGAACTTAGTTTCGAATAAACACACATAAACAAACAAA
ATGGTTAGAGTTGCTATTAAACGGTTTCGGTAGAATCGGTAGATTGGTCAT
GAGAATTGCTTTGTCTAGACCAAACGTCGAAGTTGTTGCTTTGAACGACC
CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT
CACGGTAGATACGCTGGTGAAAGTTTCCACGATGACAAGCACATCATTGT
CGATGGTAAGAAGATTGCTACTTACCAAGAAAGAGACCCAGCTAACTTGC
CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGGTGTTTTC
AAGGAATTAGACACTGCTCAAAAGCACATTGACGCTGGTGCCAAGAAGGT
TGTTATCACTGCTCCATCTTCCACCGCCCCAATGTTGTCATGGGTGTTA
ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT
ACCACCAACTGTTTGGCTCCATTGGCCAAGGTTATCAACGATGCTTTCGG
TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTCAA
AGACTGTTGACGGTCCATCCCAAGGACTGGAGAGGTGGTAGAACCGCT
TCCGGTAACATCATCCCATCCTCCACCGGTGCTGCTAAGGCTGTGGTAA
GGTCTTGCCAGAATTGCAAGGTAAGTTGACCGGTATGGCTTTCAGAGTCC
CAACCGTCGATGTCTCCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA
ACCACCTACGATGAAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA
GTTGAAGGGTGTTTTGGGTTACACCGAAGACGCTGTTGTCTCTCTGACT
TCTTGGGTGACTCTCACTCTTCCATCTTCGATGCTTCCGCTGGTATCCAA
TTGTCTCCAAAGTTCGTCAAGTTGGTCTCCTGGTACGACAACGAATACGG
TTACTCTACCAGAGTTGTCTGACTTGGTTGAACACGTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVAINGFGRIGRLVMRIALSRPNVEVVALNDPFITNDYAAAYMFKYDST
HGRYAGEVSHDDKHIIVDGKKIATYQERDPANLPWGSSNVDIAIDSTGVF
KELDTAQKHIDAGAKKVITAPSSSTAPMFVMGVNEEKYTSDLKIVSNASC
TTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDGPSHKDWRGGRTA
SGNIIPSSTGAAKAVGKVLPELQGKLTGMAFRVPTVDVSVVDLTVKLNKE
TTYDEIKKVVKAAAEGLKGVLYTEDAVVSSDFLGDSHSSIFDASAGIQ
LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

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YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)
CGACCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA
TGTATGTAACAATTTACCGTTTTGTGTAACAATTCATTCATTCATTCTT
TTGATCCTTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG
TTTGCTGGTATGATTCCCCGCCGGGCGACGGTACGGCTGTTATCCAGCG
ATGCGGGACTTCCGTCCACAGGTATCTTTTTCTCCAACCTCCAACAGAGAT
GGAAAATGAGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAAATTTGTAAT
GAAAATGGAAGTTCGGCGGTTATATAAATGGGGGGGGTTTGTGGTGACA
ATTGACTTCACTCTCCTTTCTCAAAAATCTTGGGTGTTAGGATTAGAA
GTATCTGGAACCAACCAAGAACTACAATAACAAAATAAATAAAGC
ATGTTTCAGTAGATCTACGCTCTGCTTAAAGACGTCTGCATCCTCCATTGG
GAGACTTCAATTGAGATATTTCTCACACCTTCTATGACAGTGCCTATCA
AGCTGCCCAATGGGTGGAATATGAGCAACCAACGGGGTTGTTTCATCAAC
AACAAGTTTGTTCTTCTAAACAGAACAGACCTTCGAAGTCATTAACCC
TTCCACGGAAGAAGAAATATGTCATATTTATGAAGGTAGAGAGGACGATG
TGGAAGAGGCCGTGCAGGCCGCCGACCGTGCCTTCTCTAATGGGTCTTGG
AACGGTATCGACCCTATTGACAGGGGTAAGGCTTTGTACAGGTTAGCCGA
ATTAATTGAACAGGACAAGGATGTCATTGCTTCCATCGAGACTTTGGATA
ACGGTAAAGCTATCTCTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTGATGGTAGAATGAT
TGATACTGGTAGAACCCATTTTCTTACACTAAGAGACAGCCTTTGGGTG
TTTGTGGGCAGATTATTCCTTGAATTTCCCACTGTTGATGTGGGCTGG
AAGATTGCCCCCTGCTTTGGTCAACCGGTAACACCGTCGTGTTGAAGACTGC
CGAATCCACCCCATTTGTCGCTTTGTATGTGTCTAAATACATCCACAGG
CGGGTATTCCACCTGGTGTGATCAACATTGTATCCGGGTTTGGTAAGATT
GTGGGTGAGGCCATTACAAACCATCAAAAATCAAAAAGGTTGCCTTCAC
AGGGTCCACGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGCAGGCT
TGAAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAACATTGTCTTC
GCGGACGCCGAGTTGAAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA
CTACAATTTGGTGAGGTCTGTTGTGCGGGTTCAAGGGTGATGTTGAAG
ATCTATTTTACGACAAATTCATTGAAGAGTTCAAAGCCGCTTCTGAATCC
ATCAAGGTGGGCGACCCATTCGATGAATCTACTTTCCAAGGTGCACAAAC
CTCTCAATGCAACTAAACAAAATCTTGAAATACGTTGACATTGGTAAGA
ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGGGT
TACTTCATTAAGCCAACCTGTCTTTGGTGACGTTAAGGAAGACATGAGAAT
TGTCAAAGAGGAAATCTTTGGCCCTGTTGTCACTGTAACCAAAATCAAAT
CTGCCGACGAAGTCATTAACATGGCGAACGATTCTGAATACGGGTGGCT
GCTGGTATTACACCTCTAATATTAATACCGCTTAAAGTGGCTGATAG
AGTTAATGCGGGTACGGTCTGGATAAACACTTATAACGATTTCCACCACG
CAGTTCTTTTGGTGGGTCAATGCATCTGGTTTGGGCAGGGAATGTCT
GTTGATGCTTTACAAAATACTTGCAAGTTAAAGCGGTCCGTGCCAAATT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)
MFSRSTLCLKTSASSIGRLQLRYFSHLPMTVPPIKLPNGLYEQPTGLFIN
NKFVPSKQNKTFEVINPSTEEEIICHIEGREDDVEEAVQAADRAF SNGSW
NGIDPIDRGKALYRLAELIEQDKDVIASITLDNGKAISSSRGDVLVIN
YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAW
KIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI
VGEAITNHPKIKKVAFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVF
ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES
IKVGDPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKG
YFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLA
AGIHTSNINTALKVADRVNAGTVWINTYNDFFHHA VPFGGFNASGLGREMS
VDALQNYLQVKAVRAKLDE

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YER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)

AGATAGATAGATATAGATAGATAATGGACGTAGTTATAGAACAGAAAATC
GGTAGATCGAAAACACAGGGGAAAAAGGGGGGGGGGGGGGGGAGACAGCG
CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCGAAGTTTTGCGGA
AGCTACTTTATTCCGGCCTGGAGTCAAAAGAGGAAGCTCGGTGGCAAATA
GCTTCCTCTTTGTGGCCGGGGCGCGGGGGGACGAGGCAAAAAGCAAAGAA
AAGCAAAAAAATAAAAAAACAACAAAAACAGGGGTATGAGAAAAAG
ACACGCTTTTCCACGCGCAGCAAAAAGGAAAAAGGAAAAGGAACTCTTT
ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT
GTAGTTTCTGCAAAAATAACTTAGTTTTCCTACTTTTCAAATTGAGAG
CGCAAGCAAGTGAGAAGAAAAAGCAAGTTAAAGATAAACTAAAGATAAAA
ATGTCAACCAGTCGTGAAGATTCTGTGTACCTAGCCAAGTTGGCTGAACA
GGCCGAACGTTATGAAGAAATGGTCGAAAACATGAAGACTGTTGCCTCCT
CTGGCCAAGAGTTGTCGGTCGAAGAGCGTAATTTGTTGTCTGTTGCTTAT
AAGAACGTTATTGGTGCTCGTCGTGCCTCTTGGAGAATTGTTTCTTCTAT
TGAGCAAAAGGAGGAGTCCAAGGAGAAGTCCGAACACCAGGTGAGTTGA
TTTGTTCGTACCGTTTCAAGATTGAGACCGAACTAACTAAGATCTCCGAC
GATATTTTGTCCGTGCTAGACTCCCACTTAATTCATCAGCCACCACTGG
CGAGTCCAAGGTTTTCTACTATAAGATGAAGGGTGACTACCACCGTTATT
TGGCTGAATTTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCTCT
TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC
AACTCACCCAATCCGTCTAGGTTTGGCTCTTAACCTCTCTGTCTTCTATT
ATGAAATTCAAACCTCTCCAGACAAAGCCTGCCATTTGGCCAAGCAAGCT
TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA
AGATAGCACACTTATCATGCAACTGCTAAGGGACAATTTAACCTTATGGA
CTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACAACAA
CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA
GTAA

YER177W, 267 aa (SEQ ID NO 152)

MSTSREDSVYLAKLAEQAERYEEMVENMKTVAASSGQELSVEERNLLSVAY
KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKIETELTKISD
DILSVLDShLIPsATTGESKVFYKMKGDYHRYLAEFSSGDAREKATNAS
LEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPKACHLAKQA
FDDAIAELDTLSEESYKDSLIMQLLRDNLTLWTSMDSESGQAEDQQQQQ
QHQQQQPPAAAEGEAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)

TAGTTCTATTTGGCTATATATTTTCAGAGTGACAAATCTTTAAGAGAGACA
AACTGAGAATTAGCATATAGAATCATTCATACAACTGTTTACAAACAAGT
AAGCCCAAGACAGTTCCCAACCGCTTAAAGAAGTTTTTCCTAGAGGGAGC
AAAGTTCGTTTACATTTACACACACAGTTTTTTTTTCACTTTTTTGGGCC
TCTTCCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTTCACCTCC
TATTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTCCACTTT
TTCAATAAGGAAATAGTAGGAATAATAAAAAAGGATAGTAGTAACGATA
TACGTCGACTTTCCAGACTGGTCTCGAGCCGAATTAAATACAATAGCAG
CGTTTGACTACCACATTGTAGCTCCGCTAGAATTGATCGAAAACAAAAAT
AATAACACTAATAATTATAATAATACGGTAGAATATTTCTCGTATAAAG
ATGCCTAATCTATTGTCGAGAAACCCATTCCATGGTCATCATAATGACCA
TCATCATGACCGTGAATAATTCGTCTAATAACCCGCCACAGTTGATCAGAA
GTTCTAAATCTTTCTTAACTTCATTGGTAGAAAACAAAGTAATGACTCA
CTAAGAAGCGAGAAATCTACAGATTCATGAAATCTACCACAACCACTAC
AAATTATACTACAACAACCTTAATAACAACACCCATAGCCATTCTAATG
CAACCAGTATCTCAACAACAACCTACAATAATAACTATGAAACAACCCAC
CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCTCTCC

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AAAACAAACCCACTCCATGGCAGAATTGAAAAGGTTTTTCAGACCTTCTG
TAAATAAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC
CATTCACCCCCACCTTCAAAATCAACTTCTACAGTTAATTTAAATAATCA
CTATCGTGCCCGAGCATCCTCATGGCTTTACAGACCACTATGCTCATACCC
AGTCTGCTATACCGCCAAGTACCGATTCTATCCTATCTTTGTCCAATAAT
ATTAATATATATCACGATGATTGTATTCTGGCTCAAAAATACGGGAAATT
GGGTAAGTTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA
GACCAACTGATGGTGCTACTTTTGCCGTCAAAGAATTGAGACCAAGGAAA
CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGACCCGAGAATTTTG
TATTGGTTCGACTTTACATCACCCAAATGTTATCGAACTGTTGACGTTT
TCTCTGATTCTAAACAAAATAAATACTATGAAGTTATGGAGTACTGTCCG
ATTGATTTTTTTTGTCTGTTGTATGACAGGCAAGATGTCTCGTGGCGAGAT
CAACTGTTGCTTGAAGCAATTGACTGAAGGTGTTAAATATTTACATTCTA
TGGGATTGGCACATAGAGATTTGAAATTGGATAATTGTGTCATGACTTCC
CAGGGTATTTTGAATTAATTGATTTTGGTAGTGCTGTTGTGTTTACAGATA
TCCTTTTGAAGATGGCGTAACGATGGCTCATGGAATCGTGGGTAGTGACC
CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG
TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGTATGGTGCTTAA
AAGGTTTCCATGGAAAGCCCCCTAGAGATTCTGACGATAATTTTAGATTAT
ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT
CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA
TCACAGTGAAGTGTCCGCCATCAATCAGCAACAACAGCTCATGAATCAA
ACTTGAAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG
GGTAAAAGCGATAACAAACCAGACATTGTGGAAGAAGAAACCGAAGAAAA
TAAAGAAGATGATAGCAATAATGATAAAGAAAGCACGCCAGATAATGACA
AGGAAAGTACCATCGATATTAATAAAGCAAAAATGAGAATAAAAGCACG
GTAGTTTTCAGCTAACCCAAAGTAGATGCCGATGCCGACGCTGATTG
CGATGCAATAGGTGACTCTAACGGCAGAGTGGATTGCAAGGCTAACAGTG
ACTGCAATGACAAAACGGATTGTAATGCTAACAATGACTGCAGCAATGAA
TCGGATTGTAACGCTAAAGTTGATACTAACGTCAACACTGCTGCCAACGC
TAACCCTGATATGGTTCCCCAAAACAATCCACAACAACAACAACAAC
AACAACAACAACAACAACAACAACAACAACAACAACAACACCATCAT
CACCAGCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA
ATCGAGTCAACAGCACAGAGGACCTCACCATAAAAAAATTATTCATGGCC
CATACCGTCTATTACGCTCTACTACCACATGCTTCAAGACCTATCATGTCC
CGTATACTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT
TAATGATGAATGGTTTGCCGCCATTGCTGCCTGTACCATGGATTCAAAAA
ATAAAGTTATTAGAGCGCCTGGCCATCACCATAATTGGTTAGGGAGGAA
AATGCTCACTTAGAGACCTACAAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHHDRENSSNNPPQLIRSSKSFLNFIGRKQSNDS
LRSEKSTDSMKSTTTTTNYTTTNLNNNTHSHSNATSI STNNYNNNYETNH
HHNISHGLHDYTSASPQKQTHSMAELKRFRPSVNNKLSMSQLRSKKHST
HSPPPSKSTSTVNLNNHYRAQHPHGFTDHYAHTQSAIPPSTD SILSLSNN
INIYHDDCILAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK
PNESVKEYAKKCTAEFCIGSTLHHPNVIETVDVFSDSKQNKYYEVMEYCP
IDFFAVVMTGKMSRGEINCCLKQLTEGVKYLHSMGLAHRDLKLDNCVMTS
QGILKLIDFGSAVVFRYPFEDGVTMAHGIVGSDPYLAPEVITSTKSYDPQ
CVDIWSIGIIYCCMVLKRPWKAPRSDDNFRLYCMPDDIEHDYVESARH
HEELKERKEKRQRFNLHSDCSAINQQQPAHESNLKTVQNQVPNTPASIQ
GKSDNKPDIVEEETEENKEDDSNNDKESTPDNDKESTIDIKISKNEKST
VVSANPKKVDADADADCDANGDSNGRVDCKANSDCNDKTD CNANND CSNE
SDCN AKVD TNVNTAANANPDMVPQNNPQQQQQQQQQQQQQQQQQHHH
HQHQ NQDKAHSIASDNKSSQHRGPHHKKIIHG PYRLRLRLPHASRPIMS
RILQVDPKKRATLDDIFNDEWF AAI AACTMDSKNKVIRAPGHHHTLVREE

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NAHLETYKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTGGCGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCCCTCTC
AAAACCTCCGCACAAGTCCCAGAAAAGCGGGAAAGAAATAAAACGCCACCAA
AAAAAAAAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGA
TTATCCCGTACAAGTATTTCTCAGGAGTAAAAAAACCGTTTGTTTTGGAA
TTCCCCATTTTCGCGGCCACCTACGCCGCTATCTTTGCAACAACATATCTGC
GATAACTCAGCAAATTTTGCATATTCGTGTTGCAGTATTGCGATAATGGG
AGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAGAAAATTTTGCAT
CCTTTGCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT
TTCCATCCTACATTGTTCTAATTATCTTATTCTCCTTTATTCTTTCTTA
ACATACCAAGAAATTAATCTTCTGTCATTCGCTTAAACACTATATCAATA
ATGCAATTTTCTACTGTCGCTTCTATCGCCGCTGTCGCCGCTGTCGCTTC
TGCCGCTGCTAACGTTACCACTGCTACTGTCAGCCAAGAATCTACCACTT
TGGTCACCATCACTTCTTGTGAAGACCACGTCTGTTCTGAAACTGTCTCC
CCAGCTTTGGTTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA
ATACACCACCTGGTGCCCATTGACCACTGAAGCCCCAAAGAACGGTACTT
CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT
GCTGCTCCAACCTCACTCTGTCACTCTTACACTGGTGCTGCTGCTAAGGC
TTTGCCAGCTGCTGGTGCTTTGTTGGCTGGTGCCGCTGCTTTGTTGTTGT
AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAVAVASAAANVTATVSQESTTLVTITSCEDHVCSETVS
PALVSTATVTVDVITQYTTWCPLTTEAPKNGTSTAAPVTSTEAPKNTTS
AAPTHSVTSYTGAAAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTAGTAATCAAGAAAAGAACCCTAAATCATCGGCGTCCCCTGTG
GGGCTCTCGGAAAAACCGGTCTTGACGTCCTGAAAAGATTTCCGGCAGAT
GGTCAATGGGACCAGAGAAAAATTAATCCGACATGTGGAATATTTCTCTCC
GTTAAGGTAGTGAGCGCGGATTTTTCTGATTTGTAATTATACGGGGAGC
TCTGGCCAAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG
ATTTTCTTCTGTATCATCTCTTTCTTTTCCACACCCCTTCCGGACGGT
ATTACATATTTGTTGAGAGGTTAAATGAAAAATAAAGGGGTGGAAAAATTA
AGGACGAGATGTAAGGGAAAAAGCATAAACGAAACATTATATAAAGGAGCA
CAATTTCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTTATAACGAA
ATTTCAACAAACCAGAAACAACACAAGTACTACCAATAACCACAACAAAAC
ATGTCTGACTTAGTTAAACAAGAAATTTCCAGCTGGCGACTACAAATTCCA
ATACATTGCTATCAGCCAAAAGTGATGCTGACAGTGAATCTTGTAAGATGC
CACAAACAGTTGAATGGTCCAAATTAATTTCTGAAAAACAAGAAGGTTATC
ATTACCGGTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAGCCATAT
TCCAGGTTACATCAACTACTTGGATGAATTAGTTAAGGAAAAGGAAGTTG
ACCAAGTGATCGTTGTTACTGTTGACAACCCGTTGCTAACCAAGCGTGG
GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCTCCGA
CCCAGGCTGTGCTTTACCAAATCCATTGGTTTTCGAATTAGCCGTCGGTG
ACGGTGTTTACTGGAGTGGTAGATGGGCCATGGTTGTTGAAAACGGTATC
GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC
CTCAGTCGAAAGTGTCTTGCTCATTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLVNKKFPAGDYKFQYIAISQSDADSESKMPQTVESKLI SENKKVI
ITGAPAAFSPTCTVSHIPGYINYLDLVKEKEVDQVIVVTVDNPFANQAW
AKSLGVKDTTHIKFASDPGCAFTKSIGFELAVGDGVYWSGRWAMVVENGI
VTYAAKETNPGTDVTVSSVESVLAHL

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YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)

TTGTTGCAACAATTTTGGGATGCTTCTGCGTCGTACGACCCTGTATTTAC
CTTCTCTAGCTCATCGCTTCCCAGGGTCCACGTTAATTTTCAATTTTTT
CTTGCGTGTCTGAAGATTCAGGTCTCGAGAAATTTGTCAAAAATTTTTCAC
TAGATATTAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT
AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTGCAAAGCAAAA
GCAGCATAGAAAAAAGAGAATCCCGTTTCCAGCTTTTTTCTCTTTTTTCCCA
TTCGTTTTTTCCTGATCTTTTTTTTCTGCATCGTGGCACCTAGAACAAGAGG
TACCTTCCATCCTTCGCTTAATATTTGATACGACTTTTTTTGATTTCCATT
ATTATTATTTGTTACTATTATTATTTATCATTTGGGTTTCGGTTTTTTGT
AATAATTTTCTTTTTTTTTTTTTTGGCTCTATTTCACTAAGACATCGTATAT
ATGCCAGGCCAGATAATCAGCATTCCGTTTTTGTGCGAGAACGAGGACAT
GGATAAATACTTGTGGAGTACCGCAGTTTGAAGCTCCTTCATCAGTCCA
GTAATTCCTTCCAGTCTCACAATGCGCCCTCCCACCAGTCGAACCTACCAC
CCCCATTACAATCACATGAAATACAACAACACTGGTAGCTATTACTATTA
CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC
AATCCATTAAACAGATCTATTCCATCGGCCCGTACGGGGCTTACAACCAG
AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG
ATTTAGCGCTAACAATAATTTGAACCAGCAAAAATACAAGCAATATCCCC
AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCT
CAACTGTACTACAATAGCAACGTCAATGCTCACAACAACAACAACAACAG
CAACAACAACAACAACAACAACAACAGCAACAACAACAACAATCTTT
ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC
TCGTTGACTTCTTCCACTTCTAACTCATCTCTCCATACAACCAAAGCAC
CTTCGAATACATTTTGCCGTCAACTTCGGCAGCTTCCACAAATTTATCGT
CGTCATCATCAAACAACCTCTATGCACACCAACCCAAACCACTGCAACATCG
ACATCCGCCGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTC
GCTTATCTCGGATCTACATTCTCCACCACTGTATCTTTCTTACCAGCAA
GCCAAACCTTGCTCATGTCTCTCCACCACATCTAGCTCTATTGGCACCAC
ATAAACCCACCGCAACATTACCATCCCCATCGCAAAGGGAGGATTTTTTC
GACGGCACCAAGTGAACATGTCTTCGTCCGCATCACTCTTGATGAATGATT
CTTCTTTAGGATGGGGGTCTAACCACATGAACGTATCTTCATCCTCTCAA
CCAGCATCATCAAGACCCTTTGGCATTGGAATACTGACATGAGCGTTTG
GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)

MPGQIISIPFLSQNEDMDKYLLEYRSLKLLHQSSNSFQSHNAPSHQSNYH
PHYNHMKYNNNTGSYYYYNNNNSSVNPHNQAGLQSINRSIPSAPYGAYNQ
NRANDVPYMNTQKKHHRFSANNNLNQQKYKQYPQYTSNPMVTAHLKQTP
QLYNSNVNAHNNNNNSNNNNNNNNNNNNLYNQTFSTRYFNSNSSP
SLTSSSTNSSSPYNQSTFEYILPSTSAASTNLSSSSSNNSMHTNPTTATS
TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLLMSSTTSSSIGTN
INPPQHSPSPSQREDFSTAPVNMSSSASLLMNDSSLGWGSNHMNVSSSSQ
PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)

CTGTCGATATTGGGTACTTTGTAGTGCATTATTTCCATCAATATTAGCA
GTGTCTTCCAAGGTGAACCATTCGCTGGTAAACCATAGAGTAAAAAACA
AGTGGAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA
GCAAGTTTGGCTTATGAATCAAATACAGCCCTTGTGAGAATACGATTAAT
GTAAATACCGACCAAAGATATGCTATCCATTGCATAAAATCCAACGGATG
ACCCGTGAACAATGCTAAAAATACCATAAGCACCCTGCATTTGTTTAGAA
TGGAAATACCTAAGACAATCTCAACTGCAAGGTATAGCGGCATAAAACCC
AAAAAGACTATGAAAAAAAATATGTTTGAGAACAGGTAGTAAATTTG
TGCTTTGCTTCGAATCCTTACAAGTTAACAAAATTTATAGCGTTTGCCG
GAAACATACTTTTGGAAGGGTTAGAAGAGATGATCTCATAACTAAGGTTA

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ATGGTTACAATTGGTAGTTCCTCCCTGGTATTATTTCTTTTCTTCGTAGT
TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTTGT
GCACTTTTTTTTTTGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA
AAACATAGGTTCCCAAACCTATATAAATATATATATGTATATGTATATAT
ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA
TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA
GTTCTCCTCAAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACA
CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTTCATTGA

YDR366C, 132 aa (SEQ ID NO 126)

MVTIGSSSLVLFVFFVVFQITYTALHRSRLCTFFSKIIEEGCVWYNK
KHRFPNLYKYIYVYVYILHICFEKYVNVEIIVGIPLLIKAILGIQNILE
VLLKDLGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)

TAGACGGGCTTCCACGCGCTTCCACTCATTTCTGTCTCTGGTAATGGCCG
TGGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTTCGATT
CCCTGTATAAATATAAACGTATTCTCTTGAGCCTTCTATCCTTTTGCCAC
TGTCGTCATCATTTGTTCCCTCCTTTTTTCGCTAGATAGGTTATATTAAGAT
TTGTCTTGAATTTAATATCTCAACTCAATCCAAACTCAACCGCTAATACT
ACCATGTCCCAAGTCTATTTTGATGTGCAAGCTGATGGCCAACCAATTGG
CCGTGTCGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA
ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTCGGCTACGCTGGCTCT
CCATTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC
TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACGGTGGCAAATTCAG
ATGAAAACCTCAAGAAGCACCACGACAGACCAGGTTTGTGTCCATGGCC
AACGCCGGTCCAAACACCAACGGTTCTCAATCTTCATCACCACCGTTCC
ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACG
GTTACGACATCGTTAAGAAGGTTGAGTCCTTGGGTTCTCCTTCCGGTGCC
ACCAAGGCTAGAATTGTTGTTGCCAAGTCCGGTGAATTATAACCGCTCTG
CCTGGAACAATACAGCAAAAATTGAAACGAACTATTCTCTCTTAAATTAT
ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCTTATAACTA
A

YDR154C, 116 aa (SEQ ID NO 102)

MKTSRSTTTDQVCCPWPTPVQTPTVLNSSSPPFHAGWTVSMLSLVKLLT
VTTSLRRLSPWVLLPVPPRLELLLSPVNYNRSANNNTAKIETNYSLLNY
MYMYKVCVCMTINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)

CGCTCGCTTCCAAAGAGTTATCATCATATTCTTCATCATATTCTTCCATAC
TTAAGGTGGGTAGCGAGGACCCCTCAATTCCCCCACCTCTCTGCCAGGGC
GTCATCTTTTTCTACAAAAGCCAGGCTGAGTCACGTCAGTTGCTGACCTT
GGGGGCTGCATTGTTTCTACGAATTACTCATTTGTTTCGTGCGCTTTCC
TATTGCGCGCATGACTAGGATGGAAAAAAAAAGAAGAAAAGAAAAGCGT
TGAGTATATAATAAGAAAGAAGAAAAAGTCCGAGAGAAAAGAAGCACAAA
GGTTTTTCTCGAGGAAAACAGTAAAGTTTGATACGCACATCGTTGACAT
CGCTGACTGCAATAGGAACTGAAATAGACGGCAAACCATTAGTTCATTC
GAAAGAACGTATTGTCGAGAATTATCACTCACTATATCAGAAAATTGACA
CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAGAAAA
ATGTCTACATCATCCGTACGTTTTGCATTTAGGCGGTTCTGGCAAAGTGA
GACAGGCCCAAGACGGTGCATTTCTGGGCTCCTACTTTGAAATGGGGTC
TGGTTTTCTGCTGGATTTCAGCGATATGAAGAGACCGGTGGAAAAATTTCT
GGTGCTCAAAATTTGTGCTGCTATCTACTGCGCTGATTTGGACTCGTTG
GTCTTTGTGTCATCAAGCCAAGAAACATCTTGTGGCTTCTGTCAACTCGT
TTCTTTGTCTGACCGCTGGCTATCAATTGGGTAGAATTGCCAACTACAGG

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ATACGGAATGGCGACTCTATATCGCAATTGTGTAGCTATATTCTCAGCGG
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)

MSTSSVRFAFRFRFWQSETGPKTVHFWAPTLKWGLVFAGFSDMKRPVEKIS
GAQNLSLLSTALIWTRWSFVIKPRNILLASVNSFLCLTAGYQLGRIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)

CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA
AAAAAATGGTAGGAGTAAAAGAAAAGAAAAATAAAGGTTACCCTGCAG
TTTGATAGTCGGGTAAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA
TTACCCCGATTACCCCTCATCTTGGGAGTGCCCGCTTTTATTTCTCCCG
CCAATCGGCTATTAACGGCTTTACGTCATTCCGTGGGCGGGTCAAGCGAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAAACAAAATAAG
GCCATCATATATATATATGCGGCTGCGTGCGTGTATTCTCCCGGATAATA
TGGTGCGTTGCAATTGGAGTATTGGAGAAAATTTTCTTTTCCCTTTCATT
ACGGCGGAAATACTTCATATAAAAAAAGAATACAATCAGTCTTTAAGA
CTATACGCATAAGCATTCAAGACACATAGAAACACAAACCTATATTTTAA
ATGTCAGCATCAGCTTTTAATTTTGCCTTTAGAAGATTTTGGAATAGTGA
AACAGGCCCTAAACAGTACACTTCTGGGCCCAACTTTGAAGTGGGGGC
TGGTCTTCGCAGGGCTAAATGATATTAAGAGGCCTGTTGAGAAGGTATCA
GGAGCACAAAATTTATCTTTATTAGCGACGGCACTGATTTGGACGCGTTG
GTCGTTTGTCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTTTT
TCCTGGGTGTCAGTGCAGGCTACCATCTAACAAGAATTGCTAACTTTAGG
ATACGGAACGGTGATTCTTTTAAACAGGTTATTCACATACATAATAAAGG
GGAGACTCCTGCAGCCGTCGCAGCAAAGCAAAGTGCATCCACATCGATGA
ACAAAGGTGTGATCGGTACTAATCCGCCAATAACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)

MSASAFNFAFRFRWNSETGPKTVHFWAPTLKWGLVFAGLNDIKRPVEKVS
GAQNLSLLATALIWTRWSFVIKPKNYLLASVNNFLGCTAGYHLTRIANFR
IRNGDSFKQVIHYIIKGETPAAVAARKQTASTSMNKGVIIGNPPITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)

AAGTACGATATGGTATAACTGTAACATTGAAGGACTGAAGGACTGAAGGA
CTGAAGGACTATAGTCAAGGCCAATGGGGAAGGTCCCTTCCAGGCCATT
TGCCCGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT
GGCGGGGCAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA
CGCTTATTGTGTCAACACGGAACCTTATAGTTATCATTACTAACATCGC
AACAAAGCTGCTTTTTTACTCGTTTTTAGCCACACCATAACCCCTTTAATT
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC
TGGACGTACTGTTATATATGGCATGTCTTCGCATGTCCGTCAAATTTAGC
GTTGTCTCGAACTTAGGCTGTCTTCTTGCTGTCTGTCTTCTGATAAAA
TAATATATTGGAATAAGAAAAAATAAGGAACAAGAAAGTGTGTGAGA
ATGACTTTTGAGTAATTGCGACTCTTTGGATAACTTATTCCAGGACCCCTCC
AGAGGAAGAAGAAAGTAGTAAATTCGTTGAGGCGGTGAGAACTTTGATGA
ATAGAAACGATATGGGATATCCTCCCGCCGCTGCAAATGGTACGTATTGC
TTAAAAAATCAAGTCTTTGAATGCCAAACAGTGGAATAAACAAGAA
AAGAATGTGCATGTTGCCAGCAGTAAAGAAGAAAAATTCGACTTTCACG
AGCAAAGAAGTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT
ATCAATTGTAGTAGTAAAAACAATTACAATAAAAATAATAAGCATGTGAG
AAGCTCGAACAACACTGTAAAAAATGAAATGTTTTACCGTTACAAAAAC
ACAAGAAAGTGGACAATGATCAAAGATTGGAGAACCCTTTTTTGGAGAAGC
TGGTTTAAGGCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG
GCATATCAAATTTAACGATAACGTTGAACAGTGTATTATAACTGATGAGC

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ATTTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAACAG
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAACGCAGCAAG
TAAGCGAAGTTTCTATGATTATAACAGCGTTTACGTCGCGAGTGACGCAA
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTGGAGAC
TATCAGCGTGGGCACGATGTTTCGCGATGTTCCAAGAAATGTTTTGTTACA
GGCAGGAGAAACAGATTTTCAGTAGTGTGCTTCGGGTTGACTCCGATCTCA
AGTTATCCAACATAAGTCATCATTTCCCCCGTAAAACCTTCGTCAACTTCA
AGTCATTTCGACCTTCATTTTCGAGTCGGAACTGACACTGATACTGATAC
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC
CCAACCTGCTCCTATAA

YBR050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLDNLFQDPPEEEESSKFVEAVRTLMMNRNDMGYPAAANGTYC
LKKIKSLNAKQWKINKKRMCMPLAVKKKNFDFHEQRLILNLNLWKFIKF
INCSSKNNNYNKNNKHVRSSNNTVKNENVLPLQKHKKVDNDQRLLENLFWRS
WFKARKRRDIMGKPRERHIKFNDNVEQCIITDEHFIQRLPSTRLNSTDEQ
RPCSKSELDPICIGNAASKRSFYDYNVYVASDAIITTAATAIISNSGD
YQRGHDVRDVPNRVLLQAGETDFSSVLRVDSLKLSNISHHSPVKPSSTS
SHSTFIFESETDTDTDTAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTTGACCTGGTCAGATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC
AAGAATCTACCCAAAATGTCTCGAGCATCTTGATAATTACAGTATCGTTC
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCCTATAGGAACA
TAATTGTCAAGAAAGCACAACAATTTGTCTGCAATGTCAACAGGAGTGGC
GCATTTTATGTTTTTTCATTTTTTTTTTTTTTGTGCGTGATCATTAAGCGG
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTTCGACGACTTAGTTC
GGAAAATATTTCCAGCGGATGACACCACTTGCCACAGTTGGTGACCGCCA
AATCTAAGTCACGCGCGGAACTGAAAGGTTGTGAGTATATAAGTGATCA
CTCGCTTATATAACTGACGAGGCAGAACAGGGTGCCAAAATGCTCCTCAA
TATTTTATTTCATTTGAGATTCAAGGCTTAAAGACAGCATATATAAGAATT
ATGACGGCCGCACATCCTGTTGCTCAGTTAACTGCCGAGGCATACCTAA
AGTCAGGAGAAACCCAAAATTTCAAAGTTCTCGACTCGGAAGATTGGCGT
ACTTTCGTTTCGATTGTTGTCAAATGATGAAATCTTAAACTCTCAAGCTCCA
GAAGAGCTTGCTTTCGTTTAAACCAGGACTGGATGAAAAAATATAGAGGCCA
GTCCAATTTAATTCTCTTGCCAAACTCCACTGATAAAGTGTCGAAGATTA
TGAAATACTGTAAACGATAAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC
ACCGACTTGGTTCGGAGCCTCTGTTCCGGTATTTGATGAGATTGTTCTTTC
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT
TCAAGTGTGACGCGGGTGTGCTTATGCGTGATGCGCATCAATTTTACAC
GACCATGACCATATCTTCCCATTTGGATCTGCCTTCTAGAAACAACGTGCA
AGTGGGCGGTGTAGTTTCAACAAATGCAGGTGGTTTGAACTTTTTAAGAT
ATGGGTCTCTACACGGTAATGTTTTGGGTTTGGAAGTGGTGCTACCCAAC
GGTGAGATTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA
TGACTTGAAACAATTATTCATCGGTGCAGAGGGTACTATCGGTGTCGTTA
CTGGTGTATCCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA
TTTTTTTGGTATTGAGAATTTTCGATACCGTTTCAGAAATTATTTGTCAAGGC
TAAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG
GCTCCATTGAATGTACGATAGAATACTTGAAGGACTTGCCTTTCCTCTG
GAGAACCAACACAACCTTTTATGTTCTTATTGAAACGTCAGGGTCCAATAA
GAGACACGACGATGAGAAGCTGACTGCTTTCCTCAAAGATACCACAGATT
CTAAATTAATTTTCGAGGGTATGATGGCTAAGGACAAAGCCGATTTTGAT
AGACTTTGGACCTGGAGAAAATCTGTTCCAACAGCTTGTAATTCTTACGG
TGGTATGTACAAGTATGACATGTCACCTCAATTGAAAGATTTATATTCCG
TATCTGCGGCTGTGACGGAGAGATTAAACGCAGCCGGTTTGATTGGTGAT
GCACCAAAACCAGTTGTTAAATCATGTGGTTATGGTCATGTCGGTGACGG

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AAACATCCATTTAAATATCGCGGTAAGAGAATTTACAAAACAGATTGAGG
ACTTACTAGAACCATTTGTTTATGAATATATTGCATCAAAGAAAGGTTCC
ATCAGTGCTGAGCATGGGATCGGTTTCCATAAGAAAGGTAAGTTACACTA
CACCAGAAGTGATATTGAAATTAGATTTATGAAGGATATCAAAAATCACT
ACGATCCAAATGGAATCTTAAACCCATACAAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)

MTAAHPVAQLTAEAYPKVKRNPNFVLDSEDLAYFRSILSNDEILNSQAP
EELASFNQDWMKKYRGQSNLILLPNSTDKVSIMKYCNDKKLAVVPQGGN
TDLVGASVPVFDEIVLSLRNMNKVRDFDPVSGTFKCDAGVVMRDAHQFLH
DHDHIFPLDLPSRNNCQVGGVVSTNAGGLNFLRYGSLHGNVLGLEVVLPN
GEIISNINALRKDNTGYDLKQLFIGAEGTIGVVTGVSVIAAAKPKALNAV
FFGIENFDTVQKLFVKAELSEILSAFEFMDRGSIECTIEYLKDLFPPL
ENQHNFYVLIETSGSNKRHDDEKLTAFLKDTTDSKLISEGMMAKDKADF
RLWTWRKSVPTACNSYGGMYKYDMSLQLKDLYSVSAAVTERLNAAGLIGD
APKPVVKSCGYGHVGDGNIHLNIAVREFTKQIEDLLEPFVYEYIASKKGS
ISAEHGIGFHKKGKGLHYTRSDIEIRFMKDIKNHYDPNGILNPYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAATCAACGGCCCCCTTACAGAAAACCGCGCAGGAATTTT
TCTGGTGTGTTGTTATTTTTTTTTTCTTGTACTTATCTCACTTTTCTTTT
CTAACTATTTTTTTTGCAATTTTTTTGTGTACACTTTCACACATATAG
GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT
GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAATTTTTTCA
TAGAATAAAAAACCAAGGATAACAAACATCTTCTTCGTTTCGCTTCAAAA
TAACTACAAATTAATAATGCAATTCTCTACCGTCGCTTCTATCGCTGCTA
TTGCCGCTGTTGCCCTCCGCCGCTTCTAACATTACCACTGCTACTGTCACA
GAAGAATCTACCACTTTGGTCACTATCACTTCTTGTGAGGACCACGTTTG
TTCTGAAACAGTTTCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA
ATGACGTTATCACTTAATACACCACCTGGTGTCCATTGCCAACCCTGAA
GCACCAAAGAATACCACTTCTCCAGCTCCAAGTAAAGCAACCGAAAA
GCCAACTGAAAAGCCAACCAACAAGGTTCTAGCACTCAAAGTGTACCT
CCTACACTGGTGGCGCTGTTAAGGCTTTGCCAGCTGCCGGTGCTTTGTTG
GCTGGTGCTGCCGCTTTATTGTTGTAATTTACTCAACCTTTTCTTTAATA
TATTTT TAGAAAAATGGTTAAGTACTTTTCCGTCATAACAGCTTCCACAA
AATCGTTTATTTCAATTAATAAGATATTCTGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLQLQLKSQPKSQLKSQPNKVLALKLLP
PTLVPLLRCLQPLVLCWLVLPLYCCNLLNLFNFIFLEKWLSTFPSIQLPQ
NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACAGTACA
GGCAGCAACAGCAGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC
GTGGATAGCAAGGACTAACCGAGACAGATTGAGGTCTTTTCATGCATTACC
ACCAGTAATAATATTATACGGAATAATATAGTTTATATAATATCCATAAT
CATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC
GCTTCTCCCCCTTTTGAACCTACCATTATTATCGGACCCTCTTTACCTTTGA
ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTGGGAATACATT
TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAAGCCCT
TCTAGATCCAAATATCAGGGGTAACCTCTCACAACCTGGCCAGGAACATAT
TCCAAGTTAAAAAGAAAAATAATTATTAGAAACCAATTACCAACACAAG
ATGCTAAGATCAAATTTATGCAGAGGATCTCGAATCCTTGCAAGACTGAC
CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCGAATC
GGGACATATCATCAAAACATACTTCAATAGAGATTCTACGACAATTACG

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TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAACGT
TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC
TGTATCATAACGAGAAATTGACCGCTCCTCAGGACATTCAAATTTCTGAG
GACGGAAAATCTCTAGTGGTGAAATGGAAAGATGGCGGTATCACCAGTT
CCCTTTACAATTCTTTATCGACTATAAAGGTTCCAGTTTTGTTTCGCCAG
CAACAAGAAAACAAGAATCCAGATATAGACCCCAAGTTATGGAATAAGCGC
ATCCTGAAAGATAACGTCAAGGACTTACTTTCTGTGAGCTACAACGAGTT
TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC
AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCTCCTCTGAA
GGCCTTACCATACAAAAGATCTGTGAAAGGATCGGACCCATAAGATCGAC
TGTACATGGTGAAGGTACATTTGACGTGAATGCATCCCAAGCGACAAGTG
TTAATGCCCATTATGCCAATAAAGACTTGCCGCTACATACGGATTACCA
TTTTTTAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTGCTAC
AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT
TTTATGCTACCCGTAATGTTAGAGAATCGGATTTTGAGGCTTATGAGGCT
TTACAAATTGTTCTGTAAATTATATATATGAAAACGGCGATAAGAGGTA
CTACCAATCCAAACCTTTAATCGAACATCACGACATTAACGAGGACAATA
CTCTTCTGGGTAATTATGAGGCCCTTGATTAAATGCATTAACACTCTCCA
CCATACCAAGCACCTTTCAC'TTTCGGAATTTATGATAAGCCCTCAGATCT
AAATAATAATCTGGACTTGAATTTAATTACCACCCAGCAAAAATAACAG
AGAGATTTTTGTTTAAAGTCTTTCATTAGGGGGTTGAACTTGTTCGAGAGT
CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCCGAAAAC TG
TTGTGTTATCTTTAACAACAGGAGAATTTTGCATGCTAACTCTTTAACAA
GCTCAAACCAGCAATGGTTAAAGGGTTGCTATTTGATTCTGATACTTTC
AAGAGTAAATTAAAGTTCTTGGAAGAGAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLCRGSRLARLTTPRTYTSATAAAAANRGHIIKTYFNRDSTTIT
FSMEESSKPVSVCFNNVFLRDASHSAKLVTTGELYHNEKLTAPQDIQISE
DGKSLVVWKWDGGHHQFPLQFFIDYKSSSFVSPATRKQESRYRPQLWNKR
ILKDNVVDLLSVSYNEFIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE
GLTIQKICERIGPIRSTVHGEFTFDVNASQATSVNAHYANKDLPLHTDLP
FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRESDFEAYEA
LQIVPVNYIYENGDKRYYSKPLIEHHDINEDNTLLGNYEALIKCINYS
PYQAPFTFGIYDKPSDLNNLDLNLITPAKLTERFLFKSFIRGLNLFES
HINDFNNQFRLQLPENCCVIFNNRRILHANSLTSSNQWLKGCYFDSDTF
KSKLKFLKFKPHDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTAGGGAGGAGGCGCGTGTGAAAATGGCGGCAA
ACTAAAAGAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT
TATTCAACATGTAAATACTAATACTGCAATATCGACTTATAATAATGTAT
AGTGATCCGTATATTAATAGATCTGTTTCAATTCTTTACCTTTTTTAGGAT
ATCCGTCACCCGTGATTCCGTCGGAGGTGAGCACTCGCCCAAATAAATAA
CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTT
TCTCCCATATAAACGTTTCATTCCTTTTCTTAAGTCTTTTACAGTAATTT
CAGAAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAGAAAACT
CTTACCAATTACCCCAAAAAAATCACCATCATAAAGTACTTACATATTTA
TTTTTGTTCGTTTCTCAATATAATCTACATCATCATATATATATA
ATGTCTACACAATTTAGGAAGTCTAATCATAATAGTCATAGTAGTAAAAA
ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC
CTGACTGGACGAGTGATGATTTAATTGATATAGTTCAAGAATATGATGAT
TTGGAACTATAATTGATAAAATTACTTCCGGCGCAGTGACAAGATGGGA
TGAAGTAAAGAAACCTGCTAAGAAGGAAAAATATGAAAAAAGGAGCAAC
AACACTCATATGTCCCTCAACAACATTTGCCAAATCCAGAAGATGATATT
ACATATAAGAGTTCTAATAATAGCAATTCTTTTACTTCTACAAAGCATAA

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CAGTAGTAACAATTATACTCAAGCCAGAAATAAGAAGAAGGTACAAACAC
CACGAGCTCATACAACCGGAAACATGTTAATCTCGACAAGGGGAAGCAC
GTACCATCCAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC
TGTAATACTAAACATGACGTTCTTCAAGATTCAAATGATAACAATAATG
AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAA
GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATAACAAAGAAGAACA
CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACAACCTTCTAGGA
CATCTGCTTCACAACCAAAGAAAAATGTCGTGGGCTGCAATTGCTACACCA
AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCCTCTTGAAAACGTTGCTGA
ATTGAAGAAAGAAATAAGCGATATTAAGAAGGATGACCAAAGTCTGAAG
CTAGTGAAGAAAAAGTTAATGAACAAGAAACATCTGCACAAGAACAAGAG
GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT
GGACGGAGAAGAAGTCCAAGAAGAAGCTGAAAAAAGGAACAAGTAAAAAG
AAGAGGAACAGACAGCGGAAGAGCTGGAACAAGAACAAGATAATGTTGCT
GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAGTGC
TGTTATTTTCAGAGCCTCCAGAAGATCAAGCTAATACTGTACCTCAACCAC
AACACAATCCCAACAACCACAGCAACCACAGCAACCACAGCAACCACAG
CAACCACAGCAACCACAGCAACAACAACAACCACAGCAACCACAACAACC
ACAACAACAACACTACAACAGCAACAGCAACAGCAACAACAACCAGTACAAG
CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAACTACTATACTCAA
CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA
TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC
CTCAATCACAACAACCTCAATCACAGCAAAGTCCACAAAGTCAAAAACAA
GGGAACAACGTGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC
TGGATATTCTTATCCAGGTATGTTTGATTACAAAGGATACGCTTACGGTC
AACAAATATCAGCAACTTGCTCAAAAACAGCTCAAACTAGTGGTAATGCT
AACCAATATAATTTCCAACAAGGTTATGGTCAAGCAGGCGCGAACACTGC
TGCTGCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA
CAGCTACGCGCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTTCATG
CCATACTACGCCCACTTTTACCAACAGTCAATCCCATATGGTCAACCTCA
ATACGGTGTAGCTGGTCAATATCCATACCAGTTACCAAAGAACAATTACA
ACTATTACCAAACCTCAAAACGGTCAGGAACAGCAAAGTCCAAATCAAGGT
GTTGCCCAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA
GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG
GCCAACCTGTTAACCCACAACAACAATGCAGTTCCAACAATACTATCAA
TTCCAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCCA
ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAAT
CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQFRKSNHNSHSSKKLNPALKSKIDLTLELFPDWTSDDLIDIVQEYDD
LETIIDKITSGAVTRWDEVKKPAKKEKEYEKQHSYVPQQHLPNPEDDI
TYKSSNNSNSFTSTKHNSNNYTQARNKKKVQTPRAHTTGKHVNLDKGKH
VPSKPVSNNTSWAAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEKNEK
EQEEQQQEGHNNKEEHKQIEQPSLSKKTTSTRTSASQPKKMSWAAIATP
KPKAVKKTESPLENVAELKKEISDIKKDDQKSEASEEKVNEQETSAQE
EETAEPSEENEDRVPEVDGEEVQEEAEKKEQVKEEQTAEELEQEEDNVA
APEEEVTVVEEKVEISAVISEPPEDQANTVPQPQQSQQPQQPQQPQQPQ
QPQQPQQQQQPQQPQQPQQQLQQQQQQQQQPQVQAQAQAEQQLSQNYTQ
QQQQQYAYQQQHQLQQQYLSQQQQYAYQQQQQHPQPQSQQPQSQSPQSQKQ
GNNVAAQQYYMYQNQFPQYSYPGMFDSQGYAYGQQYQQLAQNNAQTSGNA
NQYNFQQGYGQAGANTAAANLTSAAAAAASPATAHAQPQQQQPYGGSFM
PYAHFYQQSFYPGQPPQYGVAGQYPYQLPKNNYNYQTQNGQEQQSPNQ
VAQHSQSDSQKQSQQQQQQQPQGPQPEVQMONGQPVNPQQQMDFQQYYQ
FQQQQQQAIAAAAAAQQGVPIYGYDYNSKNSRGFY

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YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)

ACAAAACAGACTTAGTTATTTTATGGTATACAACAAAAGCTCGAATGAAA
GACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAAGAATAAAGTT
ACACCTATTTCTCAAGAATTCTTTTAAATCCGCTCAAGAAAGTTTAAGGG
TATTGCATAAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT
CATAATAAATACAGGCAATTTTCTCCACATATTTAAAGGTATTTTCGATCA
TTCTTGCCAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGTTGC
GCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTTTCAGTTTAAG
GTTTCGCAAAGATACCAACTGGTTTGTAAGCAGCTGAAACGGTTCGGATT
GAAATTACAGCATTTCGAGGATGTATAAAGCGATGTCAGAATGCAGGAAAA
AAAATTATTTTAAAGTGCAACACTAGATCATCCAAAACCCAGCATGAAGA
ATGAAATTAACAAAAGAAAAAAAACGACTGCTTAGTAGGAGTGTACATA
TATCCCTCCTTTAAATTTTTTTTACACTTACTTTTCCTTTTTTTTATTGAGAA
TAGAAAAGGTGCATCTCTCTCTCTCTCTCTCTATCTCTATCTCTAAGG
TTTTATTACTTTTCATAACGTATGCTATCCATCTCTTTTCCTTTTTTTTG
TTTTGTTATTCCCTTTTTTTTACTCAGTTAGATTCATACTACTATATTTAC
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTGTGCTTTATGGGGCA
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTATGTAATTCGCTAA

YLR311C, 115 aa (SEQ ID NO 284)

MKLTKEKKNDCLVGVSYPPLNFFTLTFLFLLRIEKVHLSLSLSLSLSLR
FYFHNVCYPSLFLEFCFVIPFFYSVRFILLYLHILRSFYELNILLLYGA
ENSRRQSPPGYYVIR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)

AGAGCAGAAATGATGAAGGCTGTTAGCGCCGTCCACTGATGTGCCTGGTA
GTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCGTCACCCC
AACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC
ATCTGGCTCCTTGGCAGGGCGGTTGATGGACATCAGCCGCTCCCTTAATT
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTTCGGGAAAGTACACC
AGTCAGTTTTCGCTTTTATGACTGGGTTCTAAGGTACTAGATGTGAAGTA
GTGGTGACAGAATCAGGGAGATAAGAGGGAGCAGGGTGGGGTAATGATGT
GCGATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAAGTGAGTAT
ATAAATAGGAGCCTCCCTTCCTATTGCAACTCCATAAAATTTTTTTTGT
AGCCACTTCTGTAACAAGATAAATAAAACCAACTAATCGAGATATCAAAAT
ATGGGTAGTTTTTTGGGACGCATTCGCAGTATACGACAAGAAAAAGCACGC
AGATCCAAGTGTATATGGAGGAAACCATAACAACACAGGAGACAGTAAAA
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA
GAGAACTTGCAGAGCATGAGAAGATCTTCATAGGATCACAGGACAGTTC
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCGCAGAAGTAGAAATAC
CAAAGAATGTTGACATCTCTAACATGTCGCAAGGTGAGTTTTTAAGACTT
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)

MGSFWDAFAVYDKKKHADPSVYGGNHNNTGDSKTQVMFSKEYRQPRTHQQ
ENLQSMRRSSIGSQDSSDVEDVKEGRLPAEVEIPKNVDISNMSQGEFLRL
YESLRRGE PDNKNVR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)

GAAAAACATCTCATAAATCATCCCTGGAAAAATGTCTAGTCAAACAGAAA
GAACTTTTATTGCGGTAAAACCAGATGGTGTCCAGAGGGGCTTAGTATCT
CAAATTCATCTCGTTTTTGAAAAAAGGTTACAAACTAGTTGCTATTAA
ATTAGTTAAAGCGGATGATAAATTACTAGAGCAACATTACGCAGAGCATG
TTGGTAAACCATTTTTCCCAAAGATGGTATCCTTTATGAAGTCTGGTCCC
ATTTTGGCCACGGTCTGGGAGGGAAAAGATGTGGTTAGACAAGGAAGAAC
TATCTTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

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GTGATTTCCGGTATTGACCTAGGCAGAAACGCTCTGTCACGGCAGTGATTCT
GTTGATAGCGCTGAACGTGAAATCAATTTGTGGTTTAAGAAGGAAGAGTT
AGTTGATTGGGAATCTAATCAAGCTAAGTGGATTTATGAATGAATAACTT
ATGGCATGGGAGGGTACATATGAGCGCCTTTTTTTTCTCGCTTTGGGCAG
CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG
GAGCACGATTATATAAAAAAATACCACTTATGTTGCTACCCCTATATAC
GAATTTATAATACTTAATGACGCTTCAATGACGCCTGATGTCAAATGCTT
TTGGCTCCCAGTGAAATTGCCACACTTCCTTCTTCTTTCCGAACCTTTATA
GTATCATCGAAAAATACAAGTTGGCAAAGGTCTATTACAATCGCGGAACG
TACGATGTTTCATACGGTTTCAGCGAATAGTCTTGTAAATATCCGGAAGCAT
GCCTACCGGCATTATTATAGGTAGTTCATCGCCCTTGGACTATGTAGGGG
TACAAGTAAATAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)

MAWEGTYERLFFLAGSSYHVPSLANNIMNFLEGARLYKKNTTYVATLIY
EFIILNDASMTDPVKCFWLPVKLPFLHLLSELYSIIIEKYKLAKVYYNRGT
YDVHTVSANSLVISGSMPTGIIIGSSSPLDYGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)

GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG
CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT
GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA
CCTAGACCATTGCTGTTTTGTACCTTCACGGTCCCATTAGAGACATTTTA
CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAAACAGGGTAATA
ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACCTAATCCATC
TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA
CTTTATTATTTTTTTTATATTTTTCATTTTGACAAAATTATATAGTTAGG
AAGAATACAATAGGACTGCGACAGAAACAGATAAGGGCTCTTTTTTCTTG
GGTGTGGCTGCTTTTATTCATTAAATTTAAGACTCAAGTGTGCTGCGTGAA
ATGCTCTCATACTATGAACACAATACTGCGTTCCAAACAAACAATTGCAA
TTCCGGTAGCAATGCCGCCACTACATACAACAGCGACGCCAATAATGATA
CGATCATGAATAAAAGAAAAAATGACCATTTCGAGTTTGATACACACACT
TTCTACCAAAGATCGAAGAGAACAAAACGAGATTCTGTAAGTACAAAGTT
TTCGGTCGGTTCCGGGTGTGCTAATCTTAATAACAACAACAACAACATCA
TCATCAACAACAACAACAACAATAATAATAATAAACCATAATCAT
AATAACAGCAATAATACTGCAACCTACAATAATATTCATTATAAAAAAAA
TATCGAAATATGTCCCCTGAAACCGGTTAGTATGCACCACACTATGAACA
GCCGCTTACTGAACGAATCTGAATTTTATTCTGAAACAGAAGAGTACATG
ATTCATGGTTATTTCCGGTAACACTAATCGCGACATAACAGGCACGAGTCC
TACTGGAAGTGCTAGTATTATACAACACCAGTATCATCTTCTACCATCCC
AAAGTATAATTGCATCACAAGCACCCGGTACTGCCATGGCCGCGTTGACT
AACAACAATATCGCTAACGATTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)

MLSYEHNTAFQTNNCNSGSNAATTYNSDANNDTIMNKRKNDHFEFDTHT
FYQRSKRTRKDSVSTKF SVGSGCANLNNNNNNNI I INNNNNNNNNNNNNHNH
NNSNNTATYNNIHYKKNIEICPLKPVSMHHTMNSRLLNESEFYSETEEYM
IHGYFGNTNRDITGTSPTGSASIIQHGYHLLPSQSIIASQAPGTAMAALT
NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)

GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGA
AATTGGTGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCA
ATGGTTTGATATTCAAGGCCAAAAGTTCATGTTGTTGAGAGCTGACGAT
AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTGTGTAAGAAC
TAAGCAAACCGTTATTATTGCTCATTATCCACCAACCGTACAAGCCGGTG

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AGGCCACCAAGATTGTCGAGCAATTGGCTGACTACTTGATTGGTGTTCAA
TACTAATTTATGCAGGTAAAGTTTTCTTGCCTTATACACCACCTATTCTG
GCATCTGCGGGATTTTCGCTTCCTATTTTACAAATATTTTATTGATTGACG
CTAATTATCACTGTAAAAGGCGCACTTTTTATATGTAGTCACATCCGGTA
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATACTT
ATGTTTAATTTATCTACATATTACAATCATACGAGAAACACGCAAAAACA
ATTACTTGAATACCTTCGAAAGGAGACCAATTTGGATGTACAACCCTTTTT
TCGCCCTTTTCCTTCGATATGTTATTGATAGCTTCAAAGTCCTCAGTAGA
CAAAGTAAATATTTTCCTGTTTCGTTTTGATTTCGATCGGGATTACAGATT
TTGGCAAGACAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT
CCGGGTTGAACGTTATTTTTCTTCGCAATTTCAAGGATAACCGGTTTCCTT
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHRNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLRS
QSKYFPVRFDSIGIHRFWQDNITSLDVPANNNVSGLVIFLRNFKDNRFL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTCATCATTTTGCTCAATTGTTCTCCATTTGGGTTACCTTTTT
TGCCAGTTGGTCGTACTTGAGGTTTTTCCAGAACTTGCAACCCTTGAATT
GTCCCTCTTTGCCAACAACTAATTCTCAAGGTGGTCAGGAAATATTGGTC
GGCGATGCATCTGATACTTTTCAATTGATTACTTCTTTCCTGATCTAAT
TAAGCCGATTTTGAGGCCGATTTTCAATTTCAATTATAATGTAGTTGTTG
TAAATTTTAAAGTCATTAAACCTTTTCATGATATTGATATAGATATTGGG
AACACCATCGCAGAAAGTAGAGGCCGCAAAAAAATTATGACTGTAGAAGA
AAGACGAAGACAGTTAGCTTTTACAAGTTTTGGAAGAGCGTATGGTAAACC
CTTGATATATGGATCTATATAACTTGAAATATGCTCTATTATATCGTGAT
TTAATGACGGCTGTTGGCATTTCGGTCTTTACCAAGGTAGTAGGATTTGT
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCCATATATTCCC
CAATATTAATAATTCTACTGAGAAATGGGTGAATTTTGAAATAATTGTTG
GGATTCCATCGTTGATAAAGGCTATAATATTAGGTATACAGAATGTACTA
GAAGTTCTCCTCGATGATATAGGAATCCCCATAATGGAATCTATATTTCT
ATGTACCAATATTACGATTATTCCTCATTCCATTTCAATATGTTTCATTAT
CCTATTACATTATCGATCCTTGCATTTTCAGCTTCTCTAACTTCGGTGAC
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATAATATA
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYRTIETHIFPNINNSTEKWVNFELIVGIPSLIKAILGIQNVL
EVLDDDIGIPIMESIFLCTNITIIPHSISYVLSYSYIIDPCISASSNFGD
SFYNNLCHYLTPYMIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGAAAAAGAAGAATAATTTAATTACTTTCTCAACTAAAATCTGGA
GAAAAAACGCAAATGACAGCTTCTAAACGTTCCGTGTGCTTTCTTTCTAGAATGTTCTGG
AAAGTTTACAACAATCCACAAGAACGAAAATGCCGTTGACAATGATGAAACCATCATCCA
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC
CAAGGAAATTTTTTTTCTTAGGGCTCAGAACCTGCAGGTGAAGAAGCGCTTTAGAAATCA
AAGCACAACGTAACAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTTACATTGT
CGCCTCTAAATAAATAGTTTAAGGTTATCTACCCACTATATTTAGTTGGTTCTTTTTTTT
TTCTTCTACTCTTTATCTTTTTACCTCATGCTTTTCTACCTTTCAGCACTGAAGAGTCCA
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATTGAAACTTTGAAAC
AATTAAACGCTTCTTTGGCTGACAAGTCATACATTGAAGGGTATGTTCCGATTTAGTTTA

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CTTTATAGATCGTTGTTTTCTTTCTTTTTTTTTTTTTTCTATGGTTACATGTAAAGGGAA
GTTAACTAATAATGATTACTTTTTTCGCTTATGTGAATGATGAATTTAATCTTTGGTC
CGTGTTTTATGATGGGAAGTAAGACCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA
TCACAGTATCTGACGATAGCACAGAGCAGAGTATCATTATTAGTTATCTGTTATTTTTTTT
TTCCTTTTTTTTGTTCAAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAAGT
TCTCATTACTAACAAGCAAAATGTTTTGTTTTCTCCTTTTAAATAGTACTGCTGTTTCTC
AAGCTGACGTCACTGTCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT
TCAACCACATCGCTTCCAAGCCGATGAATTCGACTCTTTCCCAGCTGCCTCTGCTGCCG
CTGCCGAAGAAGAAGAAGATGACGATGTGATTTATTCGGTTCCGACGATGAAGAAGCTG
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATG
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAAGGCCATCGAAATGGAAGGTTTGA
CCTGGGGTGCTCACCAATTTATCCCAATTGGTTTCGGTATCAAGAAGTTGCAAATTAAC
GTGTTGTGCGAAGATGACAAGGTTTCCTTGGATGACTTGCAACAAAGCATTGAAGAAGACG
AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

>YAL003W, 206 aa (SEQ ID NO 18)

MASTDFSKIETLKQLNASLADKSYIEGTAVSQADVTVFKAQFQSAYPEFSRWFNHIASKAD
EFDSPFAASAAAAEEEEDDVDLFGSDDEEADAEAEKLKAERIAAYNAKKAAPAKPAK
SIVTLDPKPDDETNLLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVS
LDDLQQSIEEDEDHVQSTDIAAMQKL

>YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)

AAAGACTACGAGAATCAATAACGAGGCTAAACTGCGTCACACATGATTGTGATTGAGTA
CTCACGTTCTCGTGTTAATCCCGCGGTCTTCTTGTCTTTACTAACTTTTCTTCTCTCATA
GCATTCTCTTGACAGTGTTTATATACATATGTACATTTATCGAGCCAATCGAGGGC
AGCAGTTTAAACATCAAGCCGGATTTGCTCACGCTACTTTGACCCCTTTTCGTTTCGACGG
AGAGAAGAAACCGGTGTTTCTTATCCTTGCCTATTCTTTCTCTCTTACGGGGTCTTAGC
CTGTTTCTCTTGATATGATAATAGGTGGAAACGTAGAAAAAAAATCGACATATAAAAGT
GGGGCAGATACTTCGTGTGACAATGGCCAATTCAAGCCCTTTGGGCAGATGTTGCCCTTC
TTCTTTCTTAAAAAGTCTTAGTACGATTGACCAAGTCAGAAAAAAAAGGAAGT
AAAAAAAGTTTAAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCAT
TCACTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCGACGTCT
CTTGGTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC
CTAAAGATGGAGAGTGCCATAAATTATCCAACGCTGCTTTACCTCTGGCAATGGGCCATG
AGATGTCAGGAATTGTTTCCAAGGTTGGTCTTAAAGTGACAAAGGTGAAGGTTGGCGACC
ACGTGGTCTGTTGATGCTGCCAGCAGTTGTGCGGACCTGCATTGCTGGCCACACTCCAAAT
TTTACAATTCCAAACCATGTGATGCTTGTGAGAGGGGAGTGAAAAATCTATGTACCCACG
CCGGTTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTCGTAGTCTCTC
AACATCACATTATCCCGGTTCCAAAGGAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC
CTCTTTCTGTCACTGGCATGCTGTTAAGATTTCTGGTTTCAAAAAAGGCAGTTCAGCCT
TGGTTCTTGGTGCAGGTCCCATTGGGTTGTGTACCATTTTGGTACTTAAGGGAATGGGGG
CTAGTAAAATTGTAGTGTCTGAAATTGCAGAGAGAAGAATAGAAATGGCCAAGAACTGG
GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCATAAATCTATAGAGATACTACGTGGTT
TGACCAAGAGCCATGATGGGTTTGATTACAGTTATGATTGTTCTGGTATTCAAGTTACTT
TCGAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG
GTCCAAAACCTGTCCCATTCCAACCAATGGATGTGACTCTCCAAGAGAAAGTTATGACTG
GTTGATCGGCTATGTTGTCGAAGCCTTCAAGAAGTTGTTTCGTGCCATCCACAACGGAG
ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT
GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTGA
CGCCTAACCAATCACGGTGAAATGAAGTAA

>YAL060W, 382 aa (SEQ ID NO 20)

MRALAYFKKGDHFTNDIPRPEIQTDDEVIIDVSWCGICGSDLHEYLDGPFIKPKDGEC
KLSNAALPLAMGHEMSGIVSKVGPVKTKVKVGDHVVDAASSCADLHCWPHSKFYNSKPC
DACQRGSENLCETHAGFVGLGVISGGFAEQVVVSQHHIIPVPKEIPLDVAALVEPLSVTWH

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AVKISGFKKGSSALVLGAGPIGLCTILVLKMGASKIVVSEIAERRIEMAKKLGVEVFNP
SKHGHKSI EILRGLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGP KPVPF
QPM DVT LQEKVMTGSIGYVVEAFEEV VRAIHNGDIAMEDCKQLITGKQRIEDGWEKGFQE
LMDHKESNVKILLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACCTACGCCAGCCGGACGCAGACAA
TAACACACACACAAAAGAGTCTTGCAGGTTCTCTTTTAGCGGCAACGGGCATGACACTAG
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGATGTTTCATCATTTTCAGG
AACTAAAGCAACGTCTGGAAAGCGTGCCAACAACGAATTTGTAGTGACAAACATGCCTC
TGGATAAAAGAAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTTT
GTAAATAGTGTATACCATAGTAGTAGTTTCAATAATATATTCCACTACTTATATGTGTT
ACCCGCATTAGAACTCTTATTGGTGGCGAAAATCGATGGCAATAAAGAACGGAAGGGGTT
TAATAGTTGTATGCTTAACATATTTTCGATTTAAATATATAAGAAACGTCGGTAGCACAA
AATTAACCTCATTATTTAGGTATGGCGGAAATACCTGATGAAACCATCCAGCAGTTTCATGG
CATTGACCAATGTGTGCGATAACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTTAA
ATGAAGCACTAAATTCCTATTATGCTTCTCAAACGGATGACCAAAAGGATAGAAGAGAGG
AAGCACATTGGAACAGACAGCAGGAGAAGGCCCTCAAGCAAGAAGCCTTCTCCACCAACT
CTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACAGGATCCT
CACAAGGTAGCAACGAGTACTTGAAAAGGAAAGGTTCTACCTCTCCTGAACCAACCAAGG
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCCAGGTTTATGAGCTTTTTCGGATATGGTAA
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGAAA
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG
AAAAAGCGAGAAGGGGTGGTCAAAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTTAGATTAGGGTCAACCATCGACG
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAACGTAGACCAGAAAAAGTCA
CAAGAGAAATTACATTTTGAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAAATCAAGGGAGGGCTCCATTAA
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG
AGTCTTATAAAGCTCCGACGAGAAAACTGGGCGGTTTTTTCAGGCCAGGGCCAAAGACTAG
GATCTCCTATCCCGGGTGAATCGTCACCTGCGGAGGTTCCAAAGAATGAGACACCCGCTG
CTCAGGACAACACCATGCCGACAATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA
GATACGCAATGGCAAAAAGAGAAAGTTTTGCACTGCAATTCCACAGATACAGTAAAGTTTT
TGTATGAGCATGTGACATCAAATGCGAACACTGACCCATCGAGGAATTTACCTTGAATT
ATGCCTTTCTATCAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC
TGAACCTCCGTTGTCTGTGCAAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAEIPDETIQQFMALTNVSHNIAVQYLSEFGDLNEALNSYYASQTDDQKDRREEAHWNRO
QEKALKQEAFFSTNSSNKAINTEHVGGCLPKPGSSQGSNEYLKRGKSTSPEPTKGSSRS
GNSNRFMSFSDMVRGQADDDDEDQPRNTFAGGETSGLEVTDFSDPNSLLKDLLEKARRGG
QMGAEENGFRDDEDHEMGANRFTGRGFRLGSTIDADEVVEDNTSQQRRPEKVTREITFW
KEGFQVADGPLYRYDDPANSFYLSELNQGRAPLKLDDVQFGQEVEVNVYKKLDESYKAPT
RKLGGFSGQGQRLGSPFPGESSPAEVPKNETPAAQEQPMPDNEPKQGDTSIQIRYANGKR
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFTLNAYAFPIKPI SNDETTLKDADLLNSVVVQ
RWA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCCAAGTAGTAACCTCATCTTTCTGAGTGTGCTATCAAATACATACTAAGGA
GAATAAACTCTTGTTATTACGTATTCTTCATCCTTATGGGTAGAGAGCGCACTGTTTTAG
TACATTTTCTAGACGTCGAAACGTAGAGCAATTGTGATAAAACAAAAAAAAGTAAGAA
GATATATGAATAGGACGTGTCGCTAGAACTAGTAAGTATATGATGGAGATATAATAAGTG
AATTATTCGATATTTAATGAACGTTCTCATTTATTTGGAAGAAATGTTTATCACGTGATG
GAGAACCAATGAGCGGCGAGTAACCTACGCGAGGAACCCGGACCGCAATAACGATTAAAGA
AGGCCCGGAAGGGAGATGCTTAAATGATTATCACTCAGTTAAAAAAGACAAATAAGAAAC
TATTGAGACTGAACCGTTTTGGTTAATTTTCAGGTGGAAACAATTGAAGACGAGCAGTAAA

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CATTATTTTATTTAGTAGTCATGTTGTCAAGAATTGTATCAAACAATGCAACACGCTCCG
TAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCCAGTGAGAACTTATG
CTACTTTGAAAAGAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA
AAACTATGAAGATTGTTGCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAATTTCCG
CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAACGCCGAAACCAAAAATTTGG
ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA
AGGGGTTGTGTGGTTCTATCCACTCTCAATTGGCTAAAGCTGTGAGAAGACATTTGAATG
ATCAACCAAACGCCGATATAGTCACTATTGGTGATAAAATTAATGCAGCTATTGAGAA
CCCATCCTAACAACATTAAATTTGTCTATTAATGGAATTGGTAAAGATGCCCCAACTTTCC
AAGAATCTGCTTTGATTGCCGATAAGTTATTGAGTGTCATGAAGGCCGGCACTTACCCAA
AGATTTCCATTTTCTACAATGACCCAGTGCTCTTCCCTATCTTTTGAACCATCTGAAAAAC
CGATCTTTAACGCCAAGACCATTGAACAATCCCCATCATTCGGCAAATTTGAGATCGACA
CGGACGCAAACGTTCCAAGAGATTTGTTTGAATATACTTTGGCTAACCAAATGTTGACAG
CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTT
CCAAGAATGCCGGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG
CTGTCATTACTAATGAAGTGGTTGATATTATTACTGGTGCTTCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSNNATRSVMCHQAQVGILYKTNPVRTYATLKEVEMRLKSIKNIKITKTMKIVA
STRLSKAEEKAKISAKKMDEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI
HSQAKAVRRHLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAPTFQESALIA
DKLLSVMKAGTYPKISIFYNDPVSSLSFEPSEKPIFNAKTIEQSPSFGKFEIDTDANVPR
DLFEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNEL
VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTC
TAGTAATGGCTTCATTTTGCCTAAGTTGGTCAAAATGTTGTGGGCGGCTTTTGTGTTGCA
CCGAGGAGCGCTCAGTTCGTTATAATACCAGTTTGGCCACTCCTAACTACTAAAGAAAT
AATAGAAAGATATATTATCATCAAAACATAATCACAATCAAAAAAATGTCTACATATGAAGGT
ATGTAATGATATATTATGAAGTAAGTTCCCCAAAGCCAATTAACCTAACCGAATTTTAATC
TGCATCATCTAGATTAGAGGAACATGGAATACAACAAACTCAAGGGATTACCAAGA
AGTAGGAGCAACTTCACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC
TATTTCAAAACTTTGGTAACACCAGTGGTGAGGGTGATGCACATTCAGATTCAACACTAC
TTTTACGATTATTATCGCAAATGCTTCCAGAATCATTAACAGGAAGAATGGTTGCAAGAAA
TGGATAAAGGCAAGAGTGCGGGCTGTCTCTGATACTTTTGCAGCCTCTTTACCACGAATCA
ATAAAAAAAGCTCAAAGCAACTGACAACCTGCTCCATTTGTTACACTAATTATTTAGAAG
ATGAGTACCCCTTAGTAGTTGAATTACCTCATTTGCCATCATAAGTTGCACTTAGAGTGTT
TGTCTGTCTGGCTATCTCGAAGTACAACATGTCCATTATGCAGAGATAATGTTATGGGCC
ACCGAATCATTAATGAGATTGATACAACCTGAAGCAGAACTGGAAGAAGATTGGGGTATGT
ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)

MLPESLQEEWLQEMDKGSAGCPDTFAASLPRINKKKLKATDNCISICYTNYLEDEYPLVV
ELPHCHHKFDLECLSVWLSRSTTCPLCRDNVMGHRIINEIDTTEAELEEDWGMYG

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAAATGTTATCCCCAGGGTCCATTAAGTCATCCAGAAAACAGATAGATGGATTG
AAGGCCGTAGGTTTGGATTTTGTCTACAAATTTGGACGAGTTTATCAAAAAGAACAGTGAT
AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG
TAGGGTATATACTTATACCACTGCTGTGACAGTGTACTAACCTATTTCTATTTTGTAG
GTAAGCTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT
TCGTTTGAAATGATATACCTCTTGGACTGGAATCTTCTGGAAGTTTTTGGAGGTTAGAA
AAGAGGAAGGCATCTCGCGCTGACAGAAAATTTGCTTATAAACAGCGATTGGCTATATCT
AAAAGAGCACTCATCGTCAGTCAGAAAAGCCATTACCTTTCAACGAAAGAGTAAAATAGAA
AAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTTCTCAAG

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GGGACAAAGAAGCTATGGCTAGGGCCGGCCAACCTGATCCTAAATTGCTACAGCAGTTAT
TCGGTGGTGGTGGTCTGACGATCCAACCTTAATGAAAGAATCCATGGCTGTTATTATGA
ATCCGGAGGTTGACTTAGAAACAAAACCTCGTTGCATTTGACAACTTTGAAATGTTGATTG
AGAACTTAGATAATGCTAATAATATCGAAAAATTTAAACTGTGGGAGCCATTGTTGGATG
TTCTTGTTCAGACGAAGGATGAAGAACTACGTGCTGCTGCTTTATCCATTATTGGAACGG
CTGTGCAAAACAACTTGGATTTCGAAAAATAATTTTCATGAAATACGACAATGGTCTGCGAA
GCCTTATCGAAATAGCTAGTGACAAGACAAAGCCACTCGACGTGAGAACAAAAGCTTTT
ACGCACTATCTAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTTTTCAAATTAA
ATGGGCTCGACTGCATAGCACCTGTATTAAGTGATAACACCGCCAAACCAAACTGAAAA
TGAGAGCCATTGCCTTATTGACCGCATATTTGTCTCATCTGTTAAGATTGATGAAAATATAA
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACGATTGAGTGCTTGTCTGACGAGA
GTAACCTGAACATCATAGATAGAGTTCTGTCTTTTCTCTCTCACCTGATATCTTCCGGAA
TAAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC
TAAAGGACAGACTTAATGAAGACGATTATTTAGCCGTAAAGTATGTATTATGA

>YBR101C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGGPDDPTLMKESMAVIMNPEVDLE
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIGTAVQNNLD
SQNNFMKYDNGRLSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNLGLDCIA
PVLSDNTAKPKLKMRAIALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDENLNIID
RVLSFSLSHLISSGIKFNEQELHKLNEGYKHIEPLKDRLNEDDYLA VKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG
AGTTTATTGTTGGTGTGTGCTATTCATATTTGAGCTGGTATTGGACGAAAGCAAGGATAAT
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA
TTTTAACCTTTTAATTAGTGGTTGGATCAAGTTTTCGAGACTATTCCAATCTGTGACTTG
TTGGATAAATAGTTTTTACTCGTTTAGTATAATCCTTTTTTCTAAAAGTGCTTAGAGTT
CTCTAAGATGTTCTTGTTTACAATGTGAGCGATTTAGGAAATTTCTTAAAAATGGCCGAG
CGGCGCTAGCATTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAAATGTGAGGGGA
CAGGGGTTATATAAGAACGAAAAATTGTCATCCTGCATTTTTTCTTTTAAAACAGCTATACA
AAAAGTGATACCGACATACAATGAAGTATCTAAACTTAGTTTTTCGTGCTTCAGCTTCTTA
TTAGCATCAAATACGCCTCATTTCGGCCGAGCCTTTTCTCTTTTTTGAAGATGATACCACCT
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAACCTTAAATTGG
ACCGTTTGAATCACGATGATCCGCTGTTTACAACCTTTTATTTCTTCTGTGGACACAGATT
ACAGTTTGAAGACTTAGAACAGTAGATCCTTCTAAACTAGGAATTGACACCGTAAACCAAT
GGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTTGAAGTA
GGAACGATCCTGCTAACGACCCCAATTATCTTTGGTTAAATGGTGGACCTGGTTGTTCTCT
CGTTTACTGGGTTGCTATTTGAACTAGGCCCTCATCAATTGGCGCCGATATGAAACCAA
TCCACAATCCCTATTCTTGAATAATAACGCTTCAATGATCTTCTTAGAACAGCCACTCG
GAGTCGGCTTTTCTATGGTGATGAAAAAGTCTCCTCTACAAAATTAGCAGGCAAAGATG
CGTACATTTTCTGGAATTGTTTTTTGAAGCTTTTCTCATTACGCTCCAACGATTTCC
ACATTGCAGGCGAATCCTATGCAGGACATTATATCCCTCAAATTGCACATGAGATCGTTG
TCAAGAACCCTGAAAGAACGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG
ACCTTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCGGGAAAGGGGGCTATCACC
CTGTTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCTGATGGT
TGAACAAGTTATGTTATGCTTCTAAATCAAGTTTACCATGCATAGTCGCCACTGCTTACT
GTGACTCTGCACTTTTGAACCGTACATTAACACAGGACTCAACGTCTATGACATTAGAG
GGCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGTCTCCGCTATGTGCGACC
AGTATATGAATTTTCTGAAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTCTG
GCTGTGATAATGACGTGTTACCCGATTTTTTGTTTACGGGCGATGGAAGTAAACCATTTTC
AACAATATATTGCTGAATTATTAAATCACACATTCCGGTATTAATATATGCGGGTGATA
AGGATTATATTTGTAATTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGGTCAGTAAAGAAACAGGTGAAG
AGTTGGGACAAGTCAAGAAGTATGGCCCTTTACCTTTTTGAGAAATATACGATGCCGGTC
ATATGGTGCCTATGATCAACCGGAGGCAAGTTTGAAATGGTCAACAGTTGGATTTCCG

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GTAATCGTGCTTTTTTCGGATCTTTCCACCTTGGAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFLQLLISIKYASFGRAFSLFEDDTTFANLDKQLKLPQNTQQTLKLDRLNHDD
PLFTTFISSVDTDYSLRLRTVDPSKLGIDTVKQWSGYMDYKDSKHFFYWFFESRNDPAND
PIILWLNGGPGCSSFTGLLFELGPSSIGADMKPIHNPYSWNNNASMIFLEQPLGVGFSYG
DEKVSSTKLAGKDAYIFLELFFFAFPHLRSNDFHIAGESYAGHYIPQIAHEIVVKNPERT
FNLTSVMIGNGITDPLIQADYYEPMACGKGGYHPVLSSEECEKMSKAAGRCRRLNKL CYA
SKSSLPCIVATAYCDSALLEPYINTGLNVYDIRGPCEDNSTDGMCTGLRYVDQYMNFP
VQETLGSDVHNYSGCDNDVFTGFLFTGDGSKPFQQYIAELLNHNIPVLIYAGDKDYICNW
LGNHAWSNLEWINKRRYQRRMLRPWVSKETGEELGQVKNYGPFTFLRIYDAGHMPYDQ
PEASLEMVNSWISGNRAFSDLSTLENAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATGCGTATTGGGCATTTTCCTATTCTGAGAAGGAGTATGAAATAAT
TGCCGAGGGTTCAGAATGCTCTTTTAGAAATAAAAAATGAATGTAAATAGTTGGAATGTAT
CTTTAAGTAGACAAATGCAGGTAAGTTTTAGTGGCCTTTGCGGATTAACAGTATGCTCTT
AGTGCAAAACACGAAAAGAGCTCCCAATCTTTGAACACAATCGACCACGGAGGAACAATA
CACGTAGAAGGGGATAACTAAAACCTTTGTCGTGCAAGAGTATTGGAGGACACACTAACAG
CAGAACTTTGCCTTCTTAACTCTTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA
AGATGATTATTTTTTTTTTCTAAAAAAGTTCCTTTCTTTGAAGATCCCCCTGATAAAA
AAGATCAAATAATGGAAACGCTAATCATAATCAAATCGGGAGGAGAATAAACGCAAGAAG
TGTGCGTTTCTAGCTGAGTAATGGTGACAAGACATAGAGTGACTGTACTCTACAATGCC
CTGAGGATATCGGTAATCATATGCGCCAAAATGACACTCATTTGACTGTTTCGTGGAGGTT
CTGGTGTGGTTTTACAACAAAGGTGGCTATTAGAGAGGACTGGAAGCTTGGATAAAATCCT
TTACGAGAATCACTTGGAGGCCAGAGCGGACTTGGCTAGAAGTTAAGCGTTATAGAAA
ATGAACTGAGTGTGGCTTTTCACTTTACTCAAAATCTTCGGATGTGCCGGAAGGTTTA
TTACTAACCCAGTCTACAATTCATTTACAGTGAGAAGTTTGACATAGAGCAGTACTTGC
CTCCCGAAGTAGATTTGAATCTGTCTGGAATCCAGAAGATTTTACATATGATATATCAG
TGGAGCCACACAAATCCAAATTGTTGAATATCGTCTGTTGAAACAGGGTGAAGAATTTA
CAATTGCAAGAGTGAAAGATGAGAACTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG
ATGAAAGTGATGTCGATATTGGTGGAATACGTTGTAATTGGAGGATGGACGATGGTAAAA
TGGAAGATGTGAGAAACATCCTTATTGTATAAACAGGGCCATATCGCATAACAATCACT
CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCATCCAAAAATCATGA
TTGATCTCACAGATTTTCAAGAACGCCCTAAATGCATGTATCTAATGCACCTGCAATTGC
CGTTAGAATTATTTATCGATAAAATCCAATCCTCTCCCTTACTACTTTTTTGGAGAAGACG
ACTTAGAATTACCAGAATACTCTCTTCGAGATAAGGCATGGGGTTCTGAAAGTATCTTTG
AATTGAAAGCCGGCACAATGAATGAAGTGACATTGCATACTAGATATATTGAGCCTTCTA
ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA
CAGGTGACAATAAAGTTTCCCGTAATCCATTTTATAAAAAAGGTCTAGGATATGAATCTC
TCTTTACAGACGATACTACATTCCGCCATTTGAACTCGACAACCTCTTCTAGTACCAATTC
CAAGGCCGTGACACAAAGGATTATTCCAAGATCAAAAAATGGTACGTTACTATGCTTACTCA
TCTCCATCATATACATTTTCTCCAAGGTATTTGGTAACAACAAGAAGAAAAGATCAGTAA
AACGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MVTRHRVTVLYNAPEDIGNHMRQNDTHLTVRGGGVVLQQRWLLERTGSLDKSFTRITWR
PRADLARSLSVIENELSGFSVYSNSSDVPERFITNPVNSFHSEKFDIEQYLPPEVDLN
LSWNPEDFTYDISVEPTQIQIVEYRLLKQGEEFTIARVKDEKLEVGVFVDASDESVDI
GGIRCNRWMDGKMERCQKTSLLYKQGHIAYNHSTTTSLYLNPIGLHPKIMIDLTD
FERPKMYLMLHLQLPLELFIDKFQSSPLLLFGEDDLELPEYSLRDKAWGSESI FELKAGTM
NEVTLHTRYIEPSNNKGDKLEVSFDPEVILACDTGDNKVS RNP FYKKGLGYESLFTDDTT
FRHLNSTLLVPIPRPDTKDYSKIKNGTLLCLLISIIYIFSKVFGNNKKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

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CATATAAGTTTACTTCACTTTTTTGGCTGACTCCTTACTTGTCTTCCCTGCACTTTGATT
TACTTTCAGAAAAATAAGATATATGTTTCTGATAAACTTTTAGGTTAGCGGAGAAGAT
GTTGCCACGAATATCATGTAATTGAAAGGCAACGAAAGGTCTATCGTTTGCCATTCAATA
TGTGATTCGACTTGTCTTTTTTTCATTGTAACAGACATGAAACGTTTCCTTTACGTCCCTAT
GAATTTTTGTTGGCTGAACTGGGCGCTGCAGGGGCTGGACGATCCAAATGCGCGGATTTT
GAACAATTATGAGAATCCGAATTAAGAAAGGGAAAAACAATTTAATAACAGGCAGACG
TGAGAGAAGAAAAGGAAACGCTGTGATATAGAAAACATACAAATCCTATTATAAGAAGC
CAGAAGAAAGCTGATACAAGATGAGTTGGGAAGGTTTTAAGAAAGCTATCAACAGAGCTG
GTCACAGTGTGATAATTAAGAATGTCGACAAGACCATTGATAAAGAGTATGACATGGAAG
AACGTCGTTATAAAGTTCTTCAAAGAGCAGGTGAGGCATTACAAAAGGAAGCCAAAGGTT
TCTTGGACTCATTGAGAGCTGTGACAGCATCACAGACTACCATTGCCGAGGTCATCTCTA
ACCTCTATGACGATTCAAATATGTTGCTGGTGGTGGTTACAACGTTGGTAACATTATTAT
TGCAATGTGTTCAAGATTTTGATAGCGAACTGTTAAGCAATTAGACGGGCCCTTAAGAG
AAACCGTACTAGATCCAATAACAAAGTTTTTCGACGATTTTCAAAGAAATTGAGGAGGCCA
TAAAAAAGAGAGACCATAAGAAACAAGACTTCGATGCTGCGAAGGCAAAGTTTCGTAGAT
TAGTGGACAAACCTGCTAAAGATGCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT
TAGCTAAAGATATTTTCGAAAATCTTAATAACCAATTGAAAACCTGAACTACCACAGTTAG
TTTCATTAAGAGTACCTTACTTTGACCCAGTTTTGAAGCTTTAATCAAGATTCAGCTAA
GGTTCTGTACTGATGGTTACACTCGTTTAGCGCAGATTCAACAATATTTGGACCAACAAT
CAAGAGACGACTATGCCAATGGGTTATTAGACACTAAAATCGAAGAATATTAGGACAAA
TGACAAGCCTAGATATTTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSVIIKNVDKTIDKEYDMEERRYKVLQRAGEALQKEAKGFLDSLRA
VTASQTTIAEVISNLYDDSKYVAGGGYNVGNYYLQCVQDFDSETVKQLDGLPLRETVLDPI
TKFSTYFKEIEEAIKKRDHKKQDFDAKAKVRRRLVDKPAKDASKLPRAEKELSLAKDIFE
NLNNQLKTELPLVSLRVPYFDPSFEALIKIQLRFCTDGYTRLAQIQOYLDQOSRDDYAN
GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGGAATAGGCGAGCGGCTGAGTGGTTCTCCAAGCTACGGTTTTTACGTGTAG
CCCCATGTGAGCAAGCCAAACAAGGGCCCTTAAAGGCGTGAATAAAAAAGGGCGGGTT
GGAAGGTCATCTGCAGCGAGATACGAAAAGATTTTTTGCCAGATTTGCGGTTGGGCGGCT
ATTTTCGGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCATTTTCTTACAGCTTTTTT
TCGTTATCGCGGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA
CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCCTGAGATCTTGCTATAGG
TTCATTTTATATATCGTCCAATAGCAATAACAATACAACAGAACTACTAGCATCTGTTT
ATAAGAAAAAGGCAAATAGTCGACAGCTAACACAGATATAACTAAACAACCACAAAACAA
CTCATATACAAACAAATAATATGTCTGACAAGGAACAAACGAGCGGAAACACAGATTTGG
AGAATGCACCAGCAGGATACTATAGTTCCCATGATAACGACGTTAATGGCGTTGCAGAAG
ATGAACGTCCATCTCATGATTCGTTGGGCAAGATTTACACTGGAGGTGATAACAATGAAT
ATATCTATATTGGGCGTCAAAAGTTTTTGAAGAGCGACTTATACCAAGCCTTTGGTGGTA
CCTTGAATCCAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCCTGCGCCCTTAG
GTCTTTTCAGCCTTCGCGTTGACGACATTTGTGCTGTCCATGTTCAATGCGAGAGCGCAAG
GGATCACTGTTTCTAATGTTGTCGTCGGTTGTGCTATGTTTTATGGTGGTTTGGTGCAAT
TGATTGCTGGTATTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCGCATTATGTT
CTTACGGTGGGTTTTGGTTGAGTTTCGCTGCAATTTACATTCCTTGGTTGGTATCTTGG
AAGCTTACGAAGACAATGAATCTGATTTGAATAATGCTTTAGGATTTTATTTGTTGGGGT
GGGCCATCTTTACGTTTGGTTAACCCTTTGTACCATGAAATCCACTGTTATGTTCTTTT
TGTTGTTCTTCTTACTAGCATTAACCTTTCTACTGTTGTCTATTGGTCACTTTGCTAATA
GACTTGGTGTACAAGAGCTGGTGGTGTCTGGGAGTTGTTGTTGCTTTTCATTGCTTGGT
ACAACGCATATGCAGGTGTTGCTACAAAGCAGAATTCATATGTACTGGCTCGTCCATTCC
CATTACCATCTACTGAAAGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)

MSDKEQTSNGNTDLENAPAGYSSHDNDVNGVAEDERPSHDSLGKIYTGDDNNEYIYIGRQ

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KFLKSDLYQAFGGTLNPG LAPAPVHKFANPAPLGLSAFALTTFVLSMFNARAQGITVPNV
VVG CAMFYGGLVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE
SDLNNALGFYLLGWAIFTFGLTVCTMKSTVMFFLLFLLALTFLLLSIGHFANRLGVTRA
GGVLGVVVAFI AWYNAYAGVATKQNSYVLARPFPLPSTERVIF

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTTGTAAAGATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCG
ATCCCGATCCCGACTCTTATTCGGATCCCTTCCGCCACATCCTGCATGTTTATTCGAATA
CCAAATTAGCTCATCTTCGTTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAAGTTTT
TTTCTAGCATCTCATCGAAAACCTTCCCTCTCCCTAATTGGCCAAAGTTTTTCATATTCATC
ATCAGTTAGAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA
AATCATATATAAGTCTGTGAGAGTCTTCAATTATTTAGCGTAACACCTATTCACCTTTCTA
ATCTTGTTTCTTGTTTTTACATTCTGCAATACAACACAACAACAAATATTAACCTCAATTA
TTATTATTTATAATTACAAAAACAACAACAAGTTTGAGACTTTAATATCTTTTGATTA
CTAAAAACAACAATTTCAAATGAACGATACGCTATCAAGCTTTTTTAAATCGTAACGAGG
CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGATT
GGTTATGGGCAGTGTTCAGTCTTTGGCTTTATATTGCTATGCTATGTTGTGATGTTCT
TCATTGCGGAGAAACAAGGGCTCCAGATTGACTAGATATGCCTTAGCTCCTGCATTTTTGA
TCACTTTCTTTGAATTTTTTGCTTTCTTCACTTATGCTTCTGATTTAGGTTGGACTGGTG
TTCAAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGGTA
TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTCTTGTCTGGCCATGCCTTTTAT
TTTTAATCGAGTTAGCCGCTAGTACTACTGGTGAGAATGACGACATTTCCGCCCTTGATA
TGGTACATTCGCTGTTAATTCAAATCGTGGGTACCTTATTCTGGGTGTTTCGCTATTAG
TTGGTTTCATTGATCAAGTCCACCTACAAGTGGGGTTATTACACCATGGTGCTGTCGCTA
TGTTGGTTACCCAAGGTGTGATATGCCAACGTCAATTCTTCAATTTGAAAAC TAGAGGGT
TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTTGGG
GCTTAAGTATGGTGGTAACCGTATTTCAACCAGACGGTGAGGCTATCTTTTATGGTGTTT
TGGATTTATGTGTATTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCGTGATT
GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCATCACCATGCTACGGACGATG
TGGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG
AGACTGCAATCCACGAACCCGAACCTGAAGCAGAGCAAGCTGTCTGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGSDWLWAVFAVFGFILLCYVVMFFIAENKG
SRLTRYALAPAFLITFFEFFAFFTYASDLGWTGVQAEFNHVKVSKSITGEVPGIRQIFYS
KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSLLIQIVGTLFWVVSLLVGS LIKS
TYKWGYTIGAVAMLV TQGVICQRQFFNLKTRGFNALMLCTCMVIVWLYFICWGLSDGGN
RIQPDGEAIFYGVLDLCVFAIYPCYLLIAVSRDGKLPRLSLTGGF SHHHATDDVEDAAPE
TKEAVPESPRASGETAIHEPEPEAEQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCCCTGCATTTCCCCATGCGTCTCGAATAGGAATTATTCAAGATGGATTATT
GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGCGTGAAACCACCTCTTTTTCACGTT
TCTTCAAGGCCAGTGCAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT
CTCAAGCCAACAGAAGTAGATAAAGCAGCCAGGAGGGTAGAGAGTGTTCAAATTATAGCA
AGCCTTCTTCTACCTGTTTTTTTTTTTGATGATTGTTTTGCGGGGTAACAATCGACTTTCGG
GCAAATTTTTTTTTTCTTTTCTCTTAACAGTATATACGGAGTGGAGAACAGACTTCCCA
TAAAAGCATATTACGTGGGGTCGTAGTAAGATTGCCGTTTATGATACCTCTATTTCAGGG
CTCAGAGCGCATCACGATCGGGAGTGTAATTCATGTGCATATAAGCAAACACACAGA
TTTCCTTTTTTCCCAGAAAAATGAGCAGTGAAATTGCCTACTCGAATACGAACACCAACA
CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAAATACAAATGCAAATGCAA
ATGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAGAGCTGA
ACCTCCCCACGGTCGATGAGCAAAGACAGTATAAGGTACAACCTGCTATTGCATATCAACA
GCATATTACTTGCTAGAGTTATTCAGATGAATAATAGTTTACAAAACAATCTACAGAACA
ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC
TTAAAAGGGTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGCCCTCAG

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CGAAACCACTGATCCTCACGCCTCCTCAGCTAGCCAACCAGCAGCAACCTCCACAGGATA
TTCTTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)

MSSEIAYSNTNTNTENENRNTGAGVDVNTNANANANATANATANATANATAELNLPTVDE
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINNSNNNNIIRIQQLISQFLKRVHAN
LQCISQINQGVPSAKPLILTPQLANQQQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGGCGTCAAGTCCTTAGACCCCAATGACAACAACACAGCCAACCGTATCATCGA
GGAATTGTTGAAGTGAATAGATAAAAAAAAAACGCACCAAGTAAGTAAGTAAATAAAGAA
TAAATAAACTATATGAGTAAACACCAAGCGAGGATGTTTCATTGTGCATCCGTGTTCTT
GATGATCACATAACTGTAAAAGAATAATACGGCACGTTAAATGTTATTTTAGAATATATA
AACACCTTATGTGCCATAAGCATTGAGCCAATCGCTGCTGTTTTTTTTTATTCCGGGGCAC
CTTCGGAAGAACACAGGCGCAATTTAGTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG
ACCGACTGCGGATCGCTTTAAGGCAAAGATAGAAGGATAAATATCTGCTTTGGAAGATAG
TCGTATCTAATTTCCCATTTCTGTTGTTTTCTTGATCTTTCCTACGCTTTCGACTTTCTTC
CTACGCGCTTTATAATAGCTATGATGTTGCCAAGATCCATGAAATTTATGACTGGAAGGA
GAATTTTCCATACTGCCACAGTAAGGGCCTTCCAGTCTACCGCTAAGAAGAGCTTAACTA
TCCCATTTTTTGCCCGTATTACCCAGAAACCAGGTGGTGTTAGGGGCACTCCCAATGATG
CCTACGTCCCCCCCCCTGAGAATAAATTAGAGGGCTCATACCACTGGTATATGGAAAAAA
TCTTTGCCTTGTCCGTCGTTCCATTGGCTACGACGGCTATGCTGACAACCGGTCCGTAT
CCACTGCAGCTGATTCTTTCTTTCTGTGCTGTTTTGGGATATTGTTACATGGAATTTA
ACTCTTGATACACCGATTATATTTCTGAAAGAGTTTATGGTGTTTGGCACAAGTACGCCA
TGTATATGTTGGGCCTTGGTTCTGCGGTCTCCCTTTTGGAACTCTATAAACTAGAAACCG
AGAATGATGGTGTGTTGGTTTAGTAAAAAGTCTATGGGATTCTTCCGAGAAAGACAACA
GTCAAAAGATTGAAGCCAAGAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)

MMLPRSMKFMTGRRIFHTATVRAFQSTAKKSLTIPFLPVLQKPGGVRGTPNDAYVPPPE
NKLEGSYHWYMEKIFALSVVPLATTAMLTTGPLSTAADSFVSVMLLGICYMEFNSCITDY
ISERVYGVWHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAATTCCAACCGGAAATTGCAAACAGCAGCAATTTCTCGTACCGATGAAGGGGAACATGG
CCGTTGTACCGAGGTTCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAACCTCGGTA
CGCTCTTCAGCTTCTTTTCGCATAATCAACGTTCTTGTTATGTAACCTACCACGTTCCATG
GCATCCGCCAACCTTGCTTCCTTACCAAATATTAATGAGCCTAAGGTGTACATTGCCGCC
GCAGGTAATATTAGCCACGACGTTGGCATTTCCTGCGCAAAGTAGCTGTTGATCTCAGT
AAAGATAACCTCAACATACTCTTTTACTTGTCTCTTTTGTAGCTAATTGCTTTCTCTCCC
CTTCTTTTCCACAAACCGCAACTATTTTTCTCTCAAAAGTTATATGAAGTATATATACTG
AATGGAGCAATTCGGGGTTGAGTGAATTACAAAATTATAGTATCTGATCAAGCACACAGT
GGAAGTGCTCGAAAAGCAATATGAGTGTGATTTGTTTCCAAATGATAGATTTGGTGCAG
AAGATAAATACGACAACCTTAAGGATGCCGTAAAAGAATGCTCCTGGCTCATCGAAGAAA
TCGTCAAACCGCAATTACCCAACATTATGACAACCTTTTCTAAATGCCTAGAGATGCTAG
AGAGTGACCAAATATTCAAATGCCTGTATCTAATGGTATTCCCAACGAAAGTAACAAAC
AAAACGACTCTCCGACGGTAAAGGGTGTATCACAAGACAAGGCCAATACATTGTTGACT
TTCACATTGTTGTCAGATTCCCACAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA
ATACGGGACTGAATTTCTTACTTATTCAATTCAGTAAGATAATGACGCACTGAAAAATA
TTTTGGAATACTGAATCAACTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT
TTGGCGTGGCCATGGAACCTTTGAACCATTTCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGGTATTCCCAGAAGATAACAACCTTGCTATGAAGGAAATGTTCCAGGATTGTTACT
CAGTCTGCGAATCCACAGCTCACATCCTAGGACTGGAACCTTACGCTTTGTAGGAATGAGC
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA
GTAAACTGGCAGGTCATTTTTCGACCAAATAAGAAATCAAGTGACAAATGAAAGAAACA

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AAACTTTATCTAAGATCCTCTCAGAAAACGGTGTACAAGTCCAGGATTCCACATTACTTA
ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGGAATTAT
TAAGAAGGGGCGTTACTTTTCGATAATAGGGTAGTCATGGAATGTGAAAAGTTAATAGTAT
CTACAAGTGATCCAACCTTTGATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA
TGGCGAACCATCAAGCAAATTTGGTAGCTAGCAAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKECSWLIEEIVKPQLPNIIDNFSKCLEMLESDQIFK
MPVSNGI PNESNKQNDSP TVKGVITRQGYIVDFHIVVRF PQFQRGKQVMFRMNTGLNFL
LIQFSKIMTHLKNILEILNQLQVATDVSEFVSKFGVAMELLNHS LILLQNPPRDLVFPED
NNFAMKEMFQDCYSVCESTAHILGLELTLCRNELCIELRNLIKVTKKPWCEIDSKTGRSF
CDQIRNQVTNERNKTL SKILSENGVQVQDSTLLNHI ISSFQSEAITLPEAQELLRRGVTF
DNRVMECEKLIVSTSDPTLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTGTGAAAAGCGAAATAGATTTCGCTGC
AAGTTTGTGAAGAAACCATCGACAAGAAATTACAAGGTTATTCCTGATGAAAAGCTGCTAA
CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAACGTCCTTGCG
TGAAGAAGTGAGCGGTTGTTCTAACCCTATTTAAAGCCGCAATTAGTAATGCAAAAAGT
TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACGGCTTTAA
CAAATATAAACTCCGAAAATCCCCACAGTGACAGAATTGGAGAAACAACCAGTTTGTATA
TCGCCATACATATAAAGAGATGTAGAAAGCATTCTTCACTGTAATGTCCAAATCGTACAT
TTGAATTTCTTGTAGGTTTATTTAAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA
TAAATTTGGAACCCTAGAAGATGTCGAAATTGGGACAAGAAAAAATGAAGTAAATTACT
CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT
TTGTCACCCAACGTATTGGGGAACATGGCCCTTTGCTTTTGAAGATTATAACTTAAATTG
ATCTTTTGGCTCATTTC AACAGGGAATAATTCCTCAAAGGAATCCACATGCTCATGGTT
CTGGTGCCTTCGGCTATTTTGAAGTAACCGATGACATTACTGATATCTGCGGGTCTGCTA
TGTTTAGTAAATTTGGGAAAAGAACGAAATGTCTAACAAGATTTTCGACTGTGGTGGGTG
ATAAAGGTAAATGCCGACACGGTTCGTGATCCAAGGGGGTTTGCCACCAAAATCTACACTG
AAGAAGGTAATTTAGATTGGGTCTACAAATAATACACCGGTATTCTTTATCAGAGACCCTT
CCAAGTTCCCTCACTTTATCCACACACAGAAGAGAAACCCACAAACCAACCTAAGGGATG
CTGACATGTTTTTGGGATTTTCTCACCCTCCTGAAAATCAGGTGGCCATTTCATCAAGTAA
TGATCCTTTTTTTCAGACCGTGGTACCCCTGCCAATACCGTAGTATGCATGGTTATTCTG
GTCATACCTATAAATGGTCCAATAAAAAACGGAGATTGGCATTATGTGCAAGTTCATATCA
AAACCGATCAAGGAATAAAGAATTTGACCATAGAAGAGGCTACCAAAATTCGGGGATCCA
ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTCAGAATGGAACTATCCTTCCT
GGACAGTTTATATTCAAACAATGACCGAACGCGATGCCAAAAAATTACCATTTTCAGTCT
TTGATTTGACTAAAGTATGGCTCAGGGGCAATTCCTTTACGGCGTGTGGGTAAGATTG
TTTTGAACGAGAATCCACTGAACCTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA
GTACCACGGTTTCCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGT
CATATGCGGATGCTCATAGATACAGGCTAGGTCCTAACTTCCATCAAATACCCGTAACT
GTCCATATGCATCTAAATTTTCAATCCCCTATCAGAGATGGACCGATGAATGTTAACG
GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC
AGGACAGACCCATTCAACAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT
GGGCAACATCCCCAGGTGATGTAGATTTCTGTCAAGCAAGAAATCTCTACCGCGTTTGG
GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTCATGTAGAAGGCG
CCTGTCTCTAAATACAGCAGCGCTTTATGATATGTTTGCTCGTGTGATAAGGGACTAT
CTGAGGCAATTAAAAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTCGAGTAACTCCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNYSVDVREDRVVTNSTGNPINEPFVTQRIGEHGPLLQDYNLIDSLAHFN
RENIPQRNPHAHGSGAFGYFEVTDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT
VRDPRGFATKFYTEEGNLDWVYNNTPVFFIIRDPSKFPHF IHTQKRNPQTNLRDADMFWDF
LTPPENQVAIHQVMILFSDRGTTPANYRSMHGYSGHYKWSNKNNGDWHYVQVHIKTDQGIK

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NLTIEEATKIAGSNPDYCCQDLFEAIQNGNYPSTVYIQTMTTERDAKKLPFSVFDLTKVW
PQQQFPLRRVGKIVLNENPLNFFAQVEQAAAFAPSTTVPYQEASADPVLQARLFSYADAH
YRLGPNFHQIPVNCPPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQ
HQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQ
RVYDMFARVDKGLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

ACTATTGTCACCTTCTCCATTGAGATTCGAAAAACCCCTCGGGTCTTGTTAGAACTAAATT
ACGTTTCATAGGGGTGGGATTTATATTGTAATTCGCGAGGTTTACACGAAAGATATCTCA
ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCACCATTGGGTATTATAGAATGTA
ATAGGTTTCAAAGCGGATATCTTTTGCCCGGTGAGTTGTTACTTTTTCATTTCGAGCAATG
AAGTACATTCTAGAAGTTCCTAGAACCTTATGGAAGCACCAAGAAAAAGGAAGTTAAAC
AAAACACTGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAAATG
TTCGTATAAATTGAACGAAACTCAAGCCAATAAAGGACTTTTCAGAGGCCTATCTCTTCT
TTCTCCACAACCTTTCGAATAAAAAACCACTAATAAAAAAGTAAATAACAAAAACAAGAAAA
AAATAAACAAAACAATAATCATGTCAAAAGCTGTTGGTATTGATTTAGGTACAACCTATT
CATGTGTTGCTCATTTTGCAAACGATAGGGTTGAAATTATCGCTAACGATCAAGGTAATA
GAACGACGCCTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCGA
AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGTCTGATCGGAC
GTAAATTCGATGATCCAGAAGTGACGAACGATGCTAAGCATTACCCATTCAAAGTGATTG
ACAAGGGAGGTAAACCGGTAGTGCAAGTGGAATATAAAGGCGAGACAAAGACATTTACTC
CAGAAGAAATTTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTGTAG
GAACAGAAGTGAAAGATGCTGTAGTAACGGTTCAGCCTATTTCAACGATTACACAAAGGC
AAGCAACAAAAGATGCCGGTACAATCGCGGGCTTGAAACGTTCTTCGTATCATTAATGAAC
CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAAACGCTC
TGATCTTTGATTTAGGTGGTGGTACTTTTGATGTCTCTCTGCTATCCATAGATGAAGGTG
TCTTTGAGGTTAAGGCTACTGCTGGTGACACTCACTTGGGTGGTGAAGATTTGATAGTA
GGCTGGTTAACTTTCTAGCCGAGGAGTTCAAAAGAAAAATAAAAAGGATCTAACAACCTA
ACCAAAGGTCCCTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAAGCTCTGTCTT
CGCTGCTCAGACATCTATAGAAATAGATTCAATTATTTGAGGGTATCGATTCTCTACTT
CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC
CAGTGGAAGAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC
TTGTTGGTGGTTCAACAAGAATTCCAAAAAGTACAAAAACTGGTTTCTGATTTTTCATG
GTAAAGAACCACCGTTTCGATTAAACCTGATGAGGCCGTCGCTTATGGTGCTGCCGTAC
AGGCTGCCATCTTAACGGGTGACCAGTCGTCGACGCCCAAGATTTACTGTTGCTGGATG
TTGCACCATTATCTCTAGGTATTGAAACTGCAGGTGGTATTATGACAAAGTTGATCCCAA
GAAATTCGACTATCCCAACAAAAAAATCGGAAGTGTTTTCACCTACGCTGACAAACCAAC
CTGGTGTTGTTGATACAAGTTTGTGAGGGTGAAAGGACAAGGACAAAAGACAACAATCTAC
TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCAAGAGGCGTACCACAAATGAAG
TTACATTTGATATCGATGCAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG
GTAAATCTAACAAGATTACAATTACTAACGATAAGGGAAGATTATCGAAGGAAGATATCG
ATAAAATGGTTGCTGAGGCAGAAAAGTTCAAGGCCGAAGATGAACAAGAAGCTCAACGTG
TTCAAGCTAAGAATCAGCTAGAATCGTACGCGTTTACTTTGAAAAATTCTGTGAGCGAAA
ATAACTTCAAGGAGAAGGTGGGTGAAGAGGATGCCAGGAAATTGGAAGCCGCCGCCCAAG
ATGCTATAAATTGGTTAGATGCTTCGCAAGCGGCTCCACCGAGGAATACAAGGAAAGGC
AAAAGGAAGCTAGAAGGTGTTGCAACCCCATTTATGAGTAAATTTTACGGAGCTGCAGGTG
GTGCCCCAGGAGCAGGCCAGTTCCGGGTGCTGGAGCAGGCCCCACTGGAGCACCAGACA
ACGGCCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQAAMN
PHNTVFDKRLIGRKFDDEVTNDKHYPFKVIDKGGKPVVQVEYKGETKTFTPEEISSM
ILTKMKETAENFLGTEVKDAVVTVPAYFNDSQRQATKDAGTIAGLNLVLRINEPTAAAI
YGLDKKSQKEHNVLIIFDLGGGTFDVSLLSIDEVFEVKATAGDTHLGGEDFDSRLVNF
LAEFKRKNKKDLTTNQRSLRRLRTAAERAKRTLSSSAQTSIEIDSLFEGIDFYTSITR
ARFEELCADLFRSTLEPVEKVLADSKLDSQIDEIVLVGGSTRIPKVQKLVSDFNNGKEPNRS

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INPDEAVAYGAAVQAAILTDGDSSTTQDLLLLDVAPLSLGIETAGGIMTKLI PRNSTIPT
KKSEVFSTYADNQPGVLIQVFEGERTRTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDA
NGILNVSAVEKGTGKSNKITITNDKGRLSKEDIDKMVAEAEKFKAEDQEQAQRVQAKNQL
ESYAFTLKNVSENNFKEKVGEEDARKLEAAQDAINWLDASQAASTEYKERQKELEGV
ANPIMSKFYGAAGGAPGAGPVPGAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACGGGGGAAGAAGAAATATCATATTCAAAGCTAATTCATTGAAATTAGTGCTTGTCTC
ATCTAGCCTTTAGTGCTTAATCTCTGGAGGAGCACATATGGGGTTAAAGCCATGCCGGGA
CTGGGGGCCCTATCGGGGCTCGAACCCGAATCCCGCGAGTATTTATTTGAAGGTCCGGG
ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGACGTTCCCTCCCCT
CACCCCTCGGCTTGTTAGAAGATCTATTGTTATAGCCTCCTCTGGAAGAATTTATGCCAG
ATGAAGAAAAAACTTCTCGAAGTTCACAGATGCCCAAATGAGGGCTTCCATCCCTGTT
AGCTGGAAGAGTGTAAGTATATCTATATAAAAAGTCGGCCTACTTTTGCCAGGTTTCGTCT
TTCACCTGCACTCTCTTGATCTTACTTTCTACTCAAAAAGAATCCAATACAAAAATAA
AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCTTCTATCATTGGCCATGG
CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCTCTGTAATCGTGGTACCATCAA
GCGATGCTACTATTGCCGGTAACGATACAGCCACGCCAGCACCAGAGCCATCATCCGCCG
CTCCAATATTCTACAACCTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA
CTACTTACTGCCCAGAACCAACGACTTTTCGTAACGAATGGCGCTACATTCACTGTTACTG
CCCCAACTACGTTAACAATTACCAACTGTCCTTGCACTATCGAGAAAGCCTACTTCAGAAA
CATCGGTTTCTTCTACACATGATGTGGAGACAAATTCTAATGCTGCTAACGCAAGAGCAA
TCCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNAKLLLSLAMASTALGLVSNSSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS
TATATQYEVVSEFTTYCPEPTTFVTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTH
DVETNSNAANARAIPGALGLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTTCGGGTCGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGACGATGA
CAAGCGCGAATCACACAAGCATGCAGAGCAAGCACGGCGTAATCGATTAGCGGTTCGCGCT
GCACGAAGTGGCGTCTTTAATCCCCGCGGAGTGGAAACAGCAAAATGTGTGCGCCGCGCC
GTCCAAAGCGACCAACCGTGGAGGCGGCCTGCCGTACATCCGTCACCTACAGCAGAACGT
GAGCAGTGACCGTGCACCAATGGGAAGCACGTTCCGGGCATATCGGACTGGGGCGCGCC
TCCCCTGCGCGGTGCTTGTATAAGAGGCGCTTTGCTGGAAAGTGGCCACACCGGGTTT
TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT
TGTATACACGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACGGA
TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAGTACTGTTGGTACTGTTGGAACAAC
TAAAGATAACCGTTGTGCCTGTTGTGGCCGCGGCCGAAGATGACGATAACGAGCAGCATG
AAGAAAAGGCAGCAGAAGGAGAAGAAAAAGAAGAAAAATGGGGATGAAGATGAGGATG
AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGATGAGGAAGAAGAGGAAGAAG
TCACTGATCAGTTGGAAGATTTGAGAGAACATTTCAAGAACACGGAGGAGGTAAGGCC
TTGTGCACCACTACGAGGAGTGTGCTGAGAGAGTCAAGATACAGCAACAACAACCCGGCT
ACGCGGATCTTGAACACAAGGAGGACTGTGTGGAGGAGTTTTTCCATCTACAGCACTATT
TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MGMLELVGEYWEQLKITVVPVAAAEDDDNEQHEEKAAEGEEKEEENGDEDEDEDEDEDD
DDDDDEDEEEEEVTDQLEDLREHFKNTEEGKALVHHYECAERVKIQQQQPGYADLEHK
EDCVVEEFFHLQHYLDTATAPRLFDKLLK

>YGR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTGGGAAAAGAACTCGTATTTTCATCCCCCTTTTTTGAAAGGGG
TGGGGAGAGACTGTTGTTTACGCCACGTCAATTATTATTTTCTTTGGCCCTGCGCTTGT
CTTATAAAATTCCGCAGCCGCCTCTTATTTTTTTTTTTTTCGATTTTTTGCCACAGGTC

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ATATTGCAAAAACCGAATGGCCGCGCCCCCTCACGCACGGGACGGAAGAAGGGCGGCGT
CCCCTGTTTTTCTGCTTTGGGCTCATCTCTTTGGGCTCCGACGGACGAAAGACGGGATTCCC
CCTCCCGTGTCTTTTTATAAATAACAAGTGCTCATTCTGCATCCTTCCTTGTTCCCGTC
GTTTGGGTACAATGCGTTGATTATCCCAACCCAAGAAAGAAAATTTGTCTCACATCTGCA
TCTGCACATTTATTTACCTATACTTTTCCATTGTTAGCAGTATTGCAAAGTGAAGAATAT
ATCAGCATCAAGTATATAGTATGCACAGAACTTACTCTTTAAGAAATTCAGGGCACCTA
CCGCCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTG
GGAAGGGTGGTCTAGCTTACAGCTTTAGGAGAAGTGCTGCTGGAGCTTTTGGCCCAGAAT
TATCCAGAAAGTTGTCTCAATTGGTTAAGATTGAAAAGAATGTTTTGAGGTCCATGGAAT
TGACAGCCAACGAAAGACGTGACGCTGCTAAGCAATTGTCTATTTGGGGGTTGGAACG
ATGACGATGTTTCCGACATCACTGATAAATTAGGTGTCTTGATCTATGAAGTTAGTGAAT
TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAAGTCCATCAGAG
ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG
CCTACTTGAAATACAAAGATCCTCAATCACCTAAGATTGAGGTCTTGGAACAAGAATTGG
TGCCTGCTGAGGCTGAATCTTTGGTCGCTGAAGCTCAATTATCTAATATCACAAGGTCAA
AGTTGAGAGCTGCTTTCAACTACCAATTTGACTCCATCATCGAACATTCAGAGAAAATTG
CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAACTATTGGACGACTCTCCTGTCACCTC
CAGGTGAAACCAGGCCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTTATTGATG
CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCCAAGTCAAGCCTACTTTAAGTT
TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAAGGCGAAGAAGAGGAAGAGGAAGACG
GTCAAGGCAGGTGGTCCGAAGACGAACAAGAAGATGGACAAATTGAAGAACCTGAACAAG
AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC
CCCAACAAACAACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPTASQLQNPPPPSTTKGRFFGKGLAYSFRRSAAGAFGPELSRKLSQ
LVKIEKNVLRSMELTANERRDAKQLSIWGLENDDDVSDITDKLGVLIYEVSELDDQFID
RYDQYRLTLKSIRDIEGSVQPSRDRDKITDKIAYLKYPQSPKIEVLEQELVRAEAS
LVAEAQLSNITRSLKRAAFNYQFDSIIHSEKIALIAGYGKALLELLDDSPVTPGETRPA
YDGYEASKQIIIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEGEEEEEDGQGRWSE
DEQEDGQIEEPEQEEEGAVEEHEQVGHQQSESLEPQQTAA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCTTGCACACCTAAAGCACATATTTTCGTTATTTTTCAC
CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAAGAAATGTTGAGAAAAAAA
TAAACCGATTCCCGTTTAGTTTTCTCCTATTTCCGTGTATATGCGTGGTTATTCGTTTTTC
GAATCCTTTTATGAATGTCCGAGGAGGTGGTACAATCCGAAATAGACTAAAGAAAAGCGA
AAGCCGTGAGTTTGTGTTGATGATAGATGACTCGCAGCTTTGTTCATCAACGGGCCACCCTA
TTCGAAGAAGGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA
TTGTTGAGAGATACATAGTGTAATCCATATCGTTCTTTTTTTTTTGTATATATCAAGCCAC
ATATCCTGTTTCTTTAATCTTTTATACGCCGTAAGAATCGGGTACTGACATAAGTGTAAG
TAGCCGTACAGAGAACAAATATGACTAAATCGGTTGGTGATGAAGAGTCACAGTACATTG
AGGACCCTAGTTTTGCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTTCGTACA
GTAATCAGCGATTTGCTGAGGGTTCCGGCCATTCTTCTGACTTAGCAAAGTCATTAGAAG
ACTATCGGCCTCCTGATGAAAAGCCGTCTCATTGTCATCTGTGGGGGAAGGTGGCGCTA
ATGAGGAAGAGAAGGGCGGTAACGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT
TTTCTCCAAGACTGCGAAATCATAGGAAAAAGATTCTCTCGAAGTTTGTTTTGAACAACT
TCTTCATTGCTTGTGTGTGTATCGCTCATATCGATTTACTGGGGTGCCGTGTACGGAA
CAGATCGTTACTTTTTCAAAGTGAAGAAATATTGTTGTATTGCAGGATGCGCCATCTAATA
CTTCAGTTCAATCTATTTCCGCGATCATACCCTCATTGTTAGCGTCTGTCCCCGGGACAT
GGCATATATACAACGCAACATCATTTTCATAGGAAATTTGGTACGACGAACTCCACCGAAA
TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTTA
AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACTCGGAGT
TCAATTCATCAATTTTTTTTGAATCCGTGTTTGAAGTGGTCGTGACCCATCGAGTGTTA
AATCGACCATTTACCACTCATGCAACAATTGGAGGTCCGCCTTCAGAAATATTACGTCA
AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

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ACATGGAGAACTGGGCGATTGCAGGACAGTTGTTGTTACCTACAACGATTATCGTCCCT
TTGCTGATCGTATTCTAATGGCCCCCTCTGCAGGTCGGTCTGATTATTGTATTTTGTAA
CCGTTTTACAACGTGTCATTATATGGTAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC
CAAAGCATATTTTAATCTACAGGCTTCTAATTTCTGGGCAACTTATTTCTTCTTTCCA
TTGGATTCTGTACCGTATCTGCAATTTTTAGGATCGATTTCACCCCCGCCTTTGGCAGAG
GAGGATTCTGTAGTATATTGGATGTCTACGTGGTTGGTAATGATGGCTGTTGGTGGTGCCA
ATGAAAACGTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTGAGTATTTGGTTGA
TGACGTGGATCATATTAAATATTTCTGCTTCATTCTACCCAATGGTTTTGAACAACGAAT
TTTACAGGTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGATTT
TTTTGAATTTAACCAAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG
CCCTCAATACATCCTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAAA
ATGCTATGCAAGCAGCAGAAGCCGCTGTGCGCAGCAGCTACCCAGCGTGCTAGCCGCCCCG
CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCGGAAATTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDEESQYIEDPSFAAAAAFTGGRDGVSYSNQRFAGSGHSSDLAKSLEDYRPPDE
KPSSLSSVGEGBANEEKGGNDGGPLARIQTGLFSPRLRNHRKKILSKFVLNNFFIACVC
VSLISIIYWGACYGTDTRYFFKVKNIVVLQDAPSNTSVQSSAISIIPLLASVPGTWHIYNAT
SFHRKFGTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLISQDANSEFNSSIFF
ESVFESGRDPSSVKSTILPLMQQLEVRQLQKYVKEYLPSLMSNITSNDRDLNINMENWAI
AGQLLFYNDYRPFADRILMAPLQVGLIYCILLTVLQLSLYGLHGMARVLKPKHILIIY
RLLIISWATYFLLSIGFCTVSAIFRIDFTPAGFRGGFVVYWMSTWLVMMAVGANENVLSL
VIAYCPPYLSIWLMTWIIILNISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVI FLNLTKR
KMGRNYGILVAWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRP AEANTDK
NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCGCTGATCCGATTACTAGCCGAAGACGTAAAAATTG
GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAAATTCAG
TCGGAGATTCCCTATTGGGCGGAATTTAGTAGATCTCTTTCCGTGCATAACGCCTGCCCCG
TTAGTCGTTATTTTCAGTTAACATTTTCTTGGCCACTGCGCTATATAAATAAATACATAT
ATATATGTCAAGCACAATAAAGAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG
AAAAGTGCCTTTTGTTCGAAGGATTAGAGTGTTCTTAATTTTAGTTTCGTTCAACGGTCTC
AAAAAAAGTGTAACAAGTAAAGCATAGCACACATCCCAAATTACAAGGCACCCTGATTA
AAAATCCAAAAATAAACCATAAGTTTTATTTTACTAAAAACATTATACGTGAAAGACAAA
CCGCATCAGAAGTTTCGAGGATGAATATTGCAGAAGAACCATCAGATGAAGTAATATCTA
GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG
ACCAATCAATAAAAAATGAAAGGAAAACCTCCACTGGTCTTCAACTGGAACAATTGGCCA
ACACAAAATTTATTAACCATAAGAATAAAATGGCAGTTACAAGAAGAAGAAGATGATCACT
GCAACTCTAGAATAACCGATCAAATAATGGACACAATACAGCACTACAAAGGTATCTCCG
TTAACAACCTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTT
TCGAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT
ACAAAGATAACGAAGAGGAAGATGATTGGAGATACGATACCGTTTTTGCAAGCACAATTCA
AGTACCCCAAGTCATTAGAAAATGCATGTACAGATATCTCGGAATTACTCAAGAGCGAAC
CTATTGGTCAGCATATTGATAAATGGTCTATCGGTGTGAACAAGCATGCACTAACCTATC
CTGGAAATATTTTTGTGCGGGGAATAGCAAAGAGCCTTTCTATTGGTGAACATAAGTTTCT
TATTTTCAAAATATGGACCAATTTTATCAATGAAATTGATATATGATAAAACGAAAGGCG
AACCTAACGGATACGGGTTTCTCTCTACCCCTTGGGTTCTCAAGCTTCACTTTGCATCA
AGGAACCTAATGGAAGGACGGTAAATGGCTCCACACTATTTATCAACTATCACGTTGAGC
GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAAACAACAATGATGATAATT
TCAGGTGTCTCTTTATAGGCAACTTGCCCTATCACAATCCTGAAAAAGTAGAGACTTTGA
TTACACCTAAAGAAGTCATAGAAGTAATCAAGAAGGAGTTATCAAAAAAGTTTCCGGACT
TTGATATCATTTTCATATTACTTTCCGAAGAGAAGTAATACAAGAAGCAGTAGTTTCAGTAA
GTTTCAATGAGGAGGGGTCAGTAGAATCAAACAAATCTTCCAATAATACTAATGGAAATG
CCCAAGATGAAGATATGTTGAAGGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG
CACTAGCAGCCATCGAGACCTTCAATGGGTTTCATGTGGCATGGAAACAGGCTCGTTGTTA

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ATAAGGCGGTTCAACATAAAGTTTACAACAACCACAATAGCCATGACAGGCACCCCTTCCA
TCAGTAACCACAATGATATGGAGGTTTGGAAATTTGCAAATAACCCAATGTATGATTACA
ATAATTATACATATGATAGATATTACTTCAACAATAATAAAAACGGGAACAGCAACGATA
CCTCCAATGTACGGTATTTTGATTCTGTAAGATCAACCCCTGTGGCAGAGAAAATGGATC
TGTTCTATCCTCAAAGGGAATCTTTCAGTGAAGGTCGTGGTCAACGTGTGCCTAGATTCA
TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATACCAA
TGAGTAATCAGCAAGAATCAAACCTATATGTCAAGCACATCCCTCTTTCTTGGACAGATG
AAGATTTATATGATTTCTACAAATCTTTCGGTGAAATAATCAGCGTTAAGGTCATTACTG
TTGGGGGTAGTAAGAACAAGTATCGTCAACAATCGAATGATAGCTCATCAGATAATGATC
TGCCAGTGGGATCATCAAGAGGTTATGGTTTTGTTTCTTTTGAAAGCCCATTAGATGCTG
CTAAGGCAATTTTGAATACAGACGGGTATCAAGTGAGCAAAGATCAAGTGTTATCTGTTT
CTTTCGCTCAGAAACGTGGTAATTTATCTTCAAGTGATGATGATGATCAATCCCAAACCTG
ATAACTCATCAAAGTTCCAAAATTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA
CAAAGTATAATAAGAAATTTATCAATGCCCTTGATGACTCAGAACCAATCGCAACAGCAAG
TCTCGAGGGAAAATTATTTTCATACCACTGCAGTACCCTAATACCAACACAAAGCCCGTGA
ACAGTTACAACCTTAATAAGTGCAAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC
CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTGCCCTATATAATACCTCCGCAGAATC
CTGCAGCAAATCATATTCCTATAATGGCAAACGGTAGTAATGAAGAGGAAGAATTTTCTA
GTGGTGATTATTCTATGGACTACTAG

>YGR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICSQOTSASAEAGDQSIKIERKTSTGLQLEQLANTNLLTI
RIKWQLQEEEDDHCNSRITDQIMDTIQHYKGISVNNSDTETYEFLPDTRRLQVLEQNKDI
YLYEHGSQEYEKSYKDNEEEDDWRYDTVLAQFKYPKSLENACTDISELLKSEPIGQHID
KWSIGVKNHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPILSMKLIYDKTKGEPNGYGF
ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNNDNFRCLFIG
NLPYHNPEKVETLITPKEVIEVIKKELSKKFPDFDIISYFYPKRSNTRSSSSVSFNEEGS
VESNKSSNNTNGNAQDEDMKGYGFIKLINHEQALAAIETFNFGFMWHGNRLVNVKAVQHK
VYNNHSTPVAEKMDLFYFPQRESFSEGRGQVRPFMGKNKFDMYQYPSTSYSLPIPMSNQQES
NLVYKHIPLSWTDLDLYDFYKSFGEIISVKVITVGGSKNKYRQQSNDSSSDNDLPVGSSR
GYGFVSFESPLDAAKAILNTDGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ
NFQPHNDYHKAYPTKYNNKFINALMTQNQSQQQVSRENYFIPLQYPNTNTKPVNSYNLIS
ANQNANWMMPMFSPFGFIPQVPPVPYIIPPQNPAANHIPIMANGSNEEEEFSSGDYSMD
Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:
570-797 (SEQ ID NO 195)

TTCTATTCCGGCTTATAAAAAGCATGGAATCCAAAAGAATTAGGCTTCTCATTCTATTTT
AATTATACTAGTACGATTCTCACTCTGTAATTTAATATCAGTGTAATATGCACCTAGTT
ATGGGTAGTTTTTGCTAACGTTACGAGCCGCGAAACTGTCCTCAATCTTCACCACTACCT
CTAATGACTGAAGAATGCTATGCGATATAACGCTGTGCGACTTTGAATATATACTTATAT
TTACATAGTTTTTCAAGTGCGTATTACTATTGCAAAGTAGTATTTTGTACAGTGATTTTGA
TCCAATTAAACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAACCATACCATTT
ATCAAGGGGACGGGATATATCACATAACAGTTTGAATGCATAATTTGTTATAGATATCTT
CTGGAATAATCTTCACAGCAAAAGCGCAAGTCGAATAATATATCGATAAATACAATCCAT
AAGACTTAAACTAACCTCAATGGCGGTAAGTATCCTATCATATTATGTGAGCTAGAACC
GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGTCTTCAAAAACCTGGTC
TACATTTCCGGTAGACTTTCTTTAAGAAGTTTAAACAGCTTATGCTCCGAATTTAATGTTAT
GGGGTGGTGCTAGCATGCTTGGGCTATTTGTATTACAGAAGGATGGCCTAAGTTTCAAG
ATACGCTATACAAAAAGATTCCGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG
AAGATAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLHFGRLSLRSLTAYAPNMLMWGGASMLGLFVFTEGWPKFQDTLYKKIP
LLGPTLEDHTPPEDKPN

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>YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

TGCTGAATTATTTTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC
AAGAATAATAGACACGCTTGGATATCCTCCATCGTGGATGATAGATATGGGTAAAAACTC
TGGAAAATTTATGAAGAAATTGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG
TATGAAAACCTATTGAAGAGTTTTGCAGAGAATACAATATAGTGGAAAAGCCCAGTAAACA
ATATTTTAAAGTGGAGAAAGTTACCAGATATTATTAGAACTACAGGTATCCTAAAAGCAT
ACAGAACTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTGTTGATCCACTT
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAGATGGACACCACAACAAGCTATGCT
ACACCCCTTCATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT
ACCGGCTCCTTCAGAAAAACATGACGATGCAAAAGGCCAGCAAAGTGAATATGGAAGTGC
GAACGACTCTAGTAACAATGCAGGCCACAACCTATGTCTATAATCCTAGCTCTGCCACTGG
TGGTGTGATAGCGTCGACATTGGTGCTATCAGTAAAAGGAAGGAGAATACATCTGGCGA
CATCTCCAATAATTTTGTCTGTTACTCATTCTGTTCAGAAGGGCCAACAAGCGCGTTCAA
TAACTTTCACATTGTCTGAAGAATAAATCGTTATTTTGTCTGACTTTTCTTAACTACCCAT
TTCATTTTATTACGGCTTGGTGCCATAATGATATACTAAATAAATATGAATTTTGCCCTTT
TCTTAATTTTCTTATACGTATAGTCATTACAATTAATAAAGTAACATTATAA

>YJL142C, 130 aa (SEQ ID NO 226)

MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIASTLVLSVKGRRIHLATSPIILL
LLILFKKGQQARSINF TLSKNKSLFCLTFLNYPFH FITAWCHNDILNKYEFCLFLIFLIR
IVITINKVTL

>YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTCGTGGTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAGGATTGC
CCATATGAAGGTATGGCGGGAAAGATAAGAAGAACAATCTGACCAAGCAAAATGTCACA
AATGTCCATCCAACAGAATACGGCCTTTACATTTTACAAAAACAAATCATCGAGGACGTT
GAGTGATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCTATAATAATTTCTT
ATTTTTCGCTTATATTTCAGGTAAATCACCATCTAACTGTATTATCTCTCACGTATCTTCA
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGCGAAAATGTTCTAGAAGG
TAATGGCAATAATAGGGATACAGATCGATCAGATCCGCCTATATAAAAGACAACGCACCG
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGGAAAAAGTCAGCAAAAACAAGA
GATAAGATAACAAGAAGAAGATGTTAAGGAGGAACTTCAACAATATACAGGACACACA
AAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCTTTGG
TAGAGGAGTCTCCCATGGGCGATTTCGGGATCAATAACCAGCCTACACAGCCTGGCGTGA
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAAACACAAGCAGTAATAATA
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCGATACGGCCACGGCAGCAGTC
TGGGTGGAGACGTTCACTCTCGCCGTTGTTTCATGA

>YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKKSNSILRSQRDQTRVDSLVEESPMGDFGINNQPTQPGVIYYFVEL
TNLGIQENTSSNNNNNNNHGDDENGSRYGHSSSLGGDVHSRRCS

>YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAATATGAAGAGTCTATTGCCAAGGATTTGAAGGCCAAAATTTTC
TCAGGTCGATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAACTGCGTTCTTGAACAAAGT
TTACAAGAGAAGCAAATAGAACTAACGCTAATCGATAAAACATTAGATTTCAAACCTAGAT
AAGGACCATGTATAAGAACTATATACTTCCAATATAATATAGTATAAGCTTTAAGATAGT
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTTTTTAAAGCCAATGAAAAT
GAAGAAATGCGTGATCGGAAATTACGGGTAGTACGAGAAGGAACTTGAGCCACCCCCCA
AATTTTATTTCATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT
GAGCAAGTCCGATTAAGAGTAAGTTGTCTGACGTTAAATACAAATAATCAACAAAACACT
ACACAAAACCTTCTACGATAATGGGTCTTCCAAGCGGTAAAACCTACATGGGATGGTGGG
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC
AAAAGCCATTACAAGGTATTTTCCATAACGCTGTATTCAATAGTTTGAAGATTTAAGT
CTCAATTTCTATATGTATTAATACCTGCGGGAATTTATTGGTACTGGTGGAAGAACGGTA
ACGAGTATAATGAATTTCTGTACAGCAAAGCTGGTAGAGAAGAGCTGGAAAGAGTTAATG